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February 8, 2005, 18:28:34; Search time 0.810811 Seconds (without alignments) 830.671 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                           Run on:
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US-10-820-200-2_COPY_161_167 Gapop 10.0 , Gapext 0.5 1 SSQDYFH 7 **BLOSUM62** Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prihted, and is derived by analysis of the total score distribution.

| | scription | alpha-amvlake (EC | amylase (| ımylase | | | | alpha-amylase (EC | | pullulanase (EC 3. | hypothetical prote | | hypothetical prote | | MEGF1 protein - ra | androgenic gland h | hypothetical prote | homeotic protein H | restriction endonu | YUP8H12.10 [import | probable virion gl | . hypothetical prote | conserved hypothet | probable membrane | thra bifunctional | aspartokinase I, h | | aspartokinase I/ho | | |
|-----------|----------------|-------------------|-----------|---------|-------|--------|--------|-------------------|--------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------------|--------------------|-------------------|-------------------|--------------------|------|--------------------|--------|-----|
| SUMMARIES | | 201 | 305 | S1 | 83 | 663 | 466 | 588 | 305 | 510 | 415 | 616 | 787 | 943 | 252 | 121 | 039 | 562 | 088 | 187 | 245 | . 199 | 248 | 146 | ÇĶ | 480 | 0629 | 502 | 658 | 803 |
| - | ü | JK0201 | A48305 | ALAS1 | ALAS3 | JS0663 | JT0466 | 3N0588 | B48305 | JC4510 | H71415 | T42616 | T18787 | T41943 | T00252 | JC7121 | B95039 | A43562 | E84088 | E86187 | S61 | T15199 | A90 | S67146 | DEECK | B85480 | B90 | ACO ACO | T17658 | 849 |
| | DB | 2 | ~ | н | Н | ~ | N | 7 | ~ | - | ~ | | | | | | | | | | | | | | | | | | | ~ |
| | ng | 478 | 498 | 499 | 499 | 499 | 499 | 499 | 499 | 624 | 130 | 420 | 601 | 1131 | 4351 | 144 | 180 | 289 | 317 | 351 | 411 | 419 | 482 | 685 | 820 | 820 | 820 | 820 | 67 | 104 |
| d | Query Match | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 85.0 | 82.5 | 82.5 | 82.5 | 82.5 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | ö | 77.5 | 7 |
| | Scor | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 34 | 33 | 33 | 33 | 33 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 31 | 31 |
| | Result No. | - | 7 | ٣ | 4 | ស | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | . 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48305
C;Accession: A88305
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asperg A;Reference number: A48305
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asperg A;Reference number: A48305
A;Accession: A48305
A;Accession: A48305
A;Residues: I-498 kKOR>
A;Residues: 1-498 kKOR>
C;Function:

| pyridoxamine 5-pho hymothetical profe | hypothetical prote RNA-binding protei | UDP-glucose pyroph UDP-N-acetylglucos | hypothetical prote RNA helicase TNZ2 | RNA helicase, ATP- hypothetical prote | <pre>fertilin alpha-II hypothetical prote</pre> | 2 | | protein F52D2.2 [i |
|---------------------------------------|--|--|---|--|---|------------------|--------|--------------------|
| B75513 AF1307 | AF1679 S72435 | F86597 H72024 | T35746 148385 | JC1087 T10575 | S55060 T03864 | S55059 AB2146 | T22209 | A89473 |
| 2 0 | 000 | ~ ~ | 77 | ~ ~ | 7 7 | 77 77 | 8 | 7 |
| 214 | 261 | 461 | 597 | 614 | 825 893 | 905 | 194 | 229 |
| 77.5 | 77.5 | 77.5 | 77.5 | 77.5 | 77.5 | 77.5 | 75.0 | 75.0 |
| 31 | 31 | 31 | 31 | 31 | 31 | 31 | 30 | 30 |
| 30 | 333 | 3.3.4 2.5.4 | 36 | 38 39 | 40 | 4 4 3 2 | 44 | 45 |

ALIGNMENTS

```
Nighternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Species: Juman-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JK0201
R;Toda, H.; Kondo, K.; Narita, K.
R;Toda, H.; Kondo, K.; Narita, K.
A;Tile: The complete amino acid sequence of Taka-amylase A.
A;Tile: The complete amino acid sequence of Taka-amylase A.
A;Reference number: JK0201
A;Molecule type: protein
A;Residues: 1-478 <-700>
A;Coss-references: UNIPROT:P10529
C;Comment: One atom of calcium per molecule is essential for the activity.
C;Comment: One atom of calcium per molecule is essential for the activity.
C;Comment: See also PIR:JT0466 and PIR:JS0240.
C;Comment: See also PIR:JT0466 and PIR:JS02040.
C;Com
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alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 SSQDYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SSODYFH 7
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A Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; glycoprotein; glycosidase; hydrolase; polyse;
F; 1-21/Domain: signal sequence #status predicted <51G>
F; 2-499/Product: alpha-amylase ore homology <AMY>
F; 194-321/Domain: alpha-amylase core homology <AMY>
F; 1-59, 171-185, 261-304, 461-496/Disulfide bonds: #status experimental
F; 142, 183, 196, 231/Binding site: calcium (Asn.) (Gu, Asp., His) #status predicted
F; 218/Binding site: carbohydrate (Asn.) (covalent) #status experimental
F; 227, 251, 318/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
                                                                                                                                                                                                                                                                                            100.0%; Score 40; DB 1;
100.0%; Pred. No. 1.5;
ive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 SSÓDYFH 168
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                                                                                                                                                                                                                                                                                                                                                                                                1 SSQDYFH 7
  A; Description:
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R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
R;Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: JS0240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-499 <WIR>
A,Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 434-443,446-447,'Q',449-458,'GTTV',459-464,467-468,'B',470,'B',472-499 <NAR>
R,Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Structure and possible catalytic residues of Taka-amylase A.
A; Reference number: A37454; MUID:84212370; PMID:6609921
A; Reference number: A37454; MUID:84212370; PMID:6609921
A; Contents: annotation; X-ray crystallography, 3.0 angstroms
B; Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkenburg, J.P.; Wilkinson, A. submitted to the Brookhaven Protein Data Bank, August 1992
A; Reference number: A51548; PDB:6TAA
                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
C;Speciae: Aspergillus oryzae
C;Speciae: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C;Accession: S04548; A33214; JS0240; A91930; A93767; A10627
R;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
A;Reference number: S04548; MUID:89237897; PMID:2785629
  A, Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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                       A Pathway: glycogen/starch degradation Cisupha-amylase core homology C; Reywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation F;194-321/Domain: alpha-amylase core homology < AMY>
                                                                                                                                                                                                     Сарв
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                                                                                                                                                                                                     ô
                                                                                                                                                  100.0%; Score 40; DB 2; Length 498; 100.0%; Pred. No. 1.5;
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A;Introne: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
                                                                                                                                                                                                   0; Indels
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A; Residues: 1-499 <GEN>
A; Genetics: AMY2
A; Note: the authors refer to this as isozyme II
R; Isemura, S: Ikenaka, T.
J. Biochem. 74, 1-10, 1973
A; Reference number: A91930; MUID:74001521; PMID:4733850
                                                                                                                                                                                                   0; Mismatches
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Best Local Similarity 100...
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A;Accession: A93767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A91930
A;Molecule type: protein
A;Residues: 206-225 <ISE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-499 <W12>
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UNDSER

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NiAlternate names: Taka-amylase A

Cipecies Aspergillus oryzae

Cipecies Aspergillus oryzae

Cipecies Aspergillus oryzae

Cipecies Aspergillus oryzae

Cipecies Sapergillus Oryzae

Ritukawa, M.; Nagaba, H.; Kirita, N.; Tsuboi, A.; Udaka, S.

Gene 84, 319-327, 1989

A; Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for mul

A; Reference number: JN0S88; MUID:90128276; PMID:2612911

A; Residues Taka-a

A; Molecule type: mRNA

A; Residues: 1-499 <-TSU

C; Comment: The alpha amylases are encoded by multigene family.

C; Comment: The alpha amylases are encoded by multigene family.

C; Comment: The alpha amylases are encoded by multigene family.

C; Comment: The alpha amylases are encoded by multigene family.

C; Comment: The alpha amylases are encoded by multigene family.

C; Comment: The alpha amylases are encoded by multigene family.

C; Comment: Taya-di

A; Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C; Function:

A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A; Pethway: glycopen(starch degradation

C; Superfamily: Aspergillus alpha-amylase; polysaccharide degradation

C; Superfamily: Aspergillus alpha-amylase; polysaccharide degradation

C; Superfamily: Aspergillus alpha-amylase; predicted <-SIG>
F; 12-10, Domain: alpha-amylase core homology <-Max>

F; 12-49, Product: alpha-amylase core homology <-Max>

F; 194-31, Domain: alpha-amylase core homology <-Max>

F; 194-31, Domain: alpha-amylase core homology <-Max>

F; 198-Binding site: carbohydrate (Asn) (covalent) #status predicted

F; 198-Binding site: carbohydrate (Asn) (covalent)
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C;Species: Aspergillus awamori
C;Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: B48305
R;Korman, D.R.; B48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.; 7
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspergance number: A48305; MUID:90254827; PMID:2340591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: B48305
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Roaduse: 1-499 «XOR»
A;Cross-references: UNIPROT:Q02906
A;Cross-references: UNIPROT:Q02906
A;Punction: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/Starch degradation
A;Pathway: glycogen/Starch degradation
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology «AMY»
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100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels
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Matches 7; Conservative
                                                                                 162 SSQDYFH 168
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Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression
A;Reference number: JS0663; MUID:92323146; PMID:1368777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: JT0466
R;Tada, S; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill A;Reference number: JT0466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Function:
A,Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A,Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A,Description: alpha-amalase alpha-amylase; core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase force homology <AMY>
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A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <MAT>
F;194-121/Domain: alpha-amylase core homology <AMY>
F;18 Binding site: carbohydrate (Asn) (covalent) #status predicted
F;231,251,318/Active site: His, Glu, Asp #status predicted
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C,Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C,Accession: J80663
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A;Molecule type: DNA
A;Residues: 1-499 <TAD>
A;Cross-references: UNIPROT:P10529
C;Comment: See also PIR:JK0201 and PIR:JK0240.
C;Comment: One atom of calcium per molecule is essential for activity.
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A,Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
Mismatches
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Best Local Similarity luv...
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7; Conservative
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                                                                                      1 SSODYFH 7
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A, Molecule type: mRNA
A, Residues: 1-499 <SHI>
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A,Cross-references: UNIPROT:039309; EMBL:AF030027; NID:g2605950; PIDN:AAC59593.1; PID:g26
A;Experimental source: strain NS80567
C;Genetics:
A;Note: 73
C;Superfamily: pseudorabies virus glycoprotein gp63
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A;Experimental source: clone BE10
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Cispecies: TS-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cispecies: TS-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Rimcharray, A.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19022
                                                                                                                                                                                                                                                                                                    envelope protein - equine herpesvirus 4 (strain NS80567)
C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Variety: strain NS80567
C;Accession: T42616
R;Telford, B.A; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J; Gen. Virol. 79, 1197-1203, 1998
A;Title: The DNA sequence of equine herpesvirus-4.
A;Reference number: Z22173; MUID:98264497; PMID:9603335
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C;Species: human herpesvirus 7
A;Variety: strain JI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41943
R;Nicholas, J.
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-420 <TEL>
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Best Local Similarity 83...
5; Conservative
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453 NSKDYFH 459
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114 NODYFH 119
SSQDYFH 7
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Matches 5; Conserv
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T41943
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                                                                                                                 Nighternate names: LKA1 protein; raw starch degrading amylase.
Nicontains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
Species: Lipowyces knonnenkoae
C;Species: Lipowyces knonnenkoae
C;Accession: JC4510; PC4116
E;Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
A;Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lipowy. Reference number: JC4510; MUID:96105202; PMID:8529895
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A;Residues: 1-624 <STE>
A;Cross-references: UNIPROT:Q01117; GB:U30376; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A;Experimental source: strain IGC4052B
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;Superfamily: lipomyces alpha-amylase core homology; glucoamylase starch
;Superfamily: lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
;1-28/Domain: signal sequence #status predicted <SIG>
;29-624/Product: alpha-amylase #status predicted <MAT>
;48-141/Domain: glucoamylase starch-binding domain homology <SBD>
;30-447/Domain: alpha-amylase core homology <AMY>
;177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted
;304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
;357,377,444/Active site: His, Glu, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
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                                                                                    pullulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Experimental source: IGC4052B
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A;Molecule type: mRNA
A;Residues: 1-144 «OKUJ>
A;Cross-references: UNIPROT:Q9U8R2; DDBJ;AB029615; GB:AB029615; NID:g6446571; PID:g64465
A;Experimental source: androgenic gland
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C;Species: Armadillidium vulgare (common pill bug)
C;Date: 32-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: JC7121
R;Okuno, A.; Hasegawa, Y.; Ohira, T.; Katakura, Y.; Nagasawa, H.
Biochem: Biophys. Res. Commun. 264, 419-423, 1999
A;Title: Characterization and cDNA cloning of androgenic gland hormone of the terrestria
A;Reference number: JC7121; MUID:20001935; PMID:10529379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-4351 cNAK>
A;Cross-references: UNIPROT:O88277; EMBL:AB011527; NID:g3449285; PIDN:BAA32458.1; PID:g3
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T00252
R;Nakayama, M:; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
R;Nakayama, M:; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T00252
submitted to the EMBL Data Library, December 1995
A;Description: Determination and analysis of the complete nucleotide sequence of human 1 Reference number: Z22022
A;Reference number: Z22022
A;Reference number: Z22022
A;Accession: T41943
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rotatus: preliminary; translated from GB/EMBL/DDBJ
A;Rotatus: DNA
A;Residues: 1-1131
A;Reperimental source: strain JI
C;Genetics:
A;Note: U41
C;Superfamily: herpesvirus DNA-binding protein
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Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
Accession: T00252
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Pred. No. 4.6e+02;
1; Mismatches 1; Indels
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Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
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MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4; Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Udaka S.; "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple related genes."; Gene 84:319-327(1989).
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MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
Brzozowski A.m., Davies G.J.;
Brzozowski A.m., Davies G.J.;
Structure of the Aspergillus oryzae alpha-amylase complexed with the inhibitor acarbose at 2.0-A resolution.";
Biochemistry 35:10837-10845(1997).
-!- CATALYMIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
                                                                                                                                                                                                                                                                                        MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6; Genes M.J., Dove M.J., Seligy V.L.; Genes M.J., Dove M.J., Seligy V.L.; Mappergillus oryzae has two nearly identical Taka-amylase genes, each containing eight introns."; Gene 79:107-117(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 206-225.
MEDILTE-74061521; Ubbed-4733850;
Temura S., Ikenaka T.;
"The amino acid sequences of glycopeptides obtained from Taka-amylase
                                                                                                                                                                                                                                                                                                                                                                                                       Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.; "Cloning and nucleotide sequence of the genomic Taka-amylase A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-80227691; PubMed-6156152;
Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
"Molacular structure of taka-amylase A. I. Backbone chain folding at
"A resolution.";
J. Biochem. 87:1555-1558(1980).
                                    Aspergillus oryzae.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                              STRAIN=DSM 63303;
BDELINE=B8237897; PubMed=2785629;
Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.;
"Three alpha-amylase genes of Aspergillus oryzae exhibit identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
MEDLINE=84212370; PubMed=6609221;
Mateuura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possable catalytic residues of Taka-amylase A.";
J. Biochem. 95:697-702(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toda H., Kondo K., Narita K., "The complete amino acid sequence of Taka-amylase A."; Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975)
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Biochem. 74:1-10(1973).
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Mol. Microbiol. 3:3-14(1989)
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                                                                                     NCBI_TaxID=5062;
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                    Name=AMY3;
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AMYA ASPOR STANDELL.
P10529; P11763; Q00250;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45) (TAA) (1,4-
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Eukaryota; Pungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=40384;
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                                Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (B similarity).
Calcium 2 (By similarity).
By similarity.
By similarity.
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By similarity.
N-linked (GlcNAC. . .) (Potential)
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Calcium 1 (via carbonyl oxygen)
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submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: Balongs to family 13 of glycosyl hydrolases.
EMBL; AB109455; BaD01051.1; -.
GO; GG:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006649; Alpha amylast sub.
InterPro; IPR006649; Alpha amylast sub.
InterPro; IPR00644; Alpha amylase; 1.
PRMINS; PR00110; ALPHAAMYLASE.
                                                                                                                                                                                                                                                        Query Match
100.0%; Score 40; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels
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SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
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Last annotation update)
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                      similarity)
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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MEDLINE-90254827; PubMed-2340591;
Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus awamori.
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
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01-007-1996 (Rel. 34, Last sequence update)
25-007-2004 (Rel. 45, Last annotation update)
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Best Local Similarity 100.
Matches 7; Conservative
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at high concentrations.

-1- SUBGUNT: Monomer.

-1- SUBGUNT: Monomer.

-1- SUBGUNT: Monomer.

-1- SUBGUNT: Monomer.

-1- BIOTECHNOLOGY: Used in the brewing industry to increase the fermentability of beer worts (including those made from unmalted cereals), in the starch industry to make high maltose and high DE syrups (starch saccharification), in the alcohol industry for reduce fermentation time, in the cereal food industry for flour supplementation and improvement of chilled and frozen dough, and in the forestry industry for low-temperature modification of starch. Sold under the name Fungamyl by Novozymes.

-1- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.

-1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X12725; CAA31219.1; -.

REMBL; X12725; CAA31219.1; -.

REMBL; X12725; CAA31219.1; -.

REMBL; X12727; CAA31220.1; -.

REMBL; M3218; AAA32708.1; -.

REMBL; M33218; AAA32708.1; -.

REMBL; M33218; AAA32708.1; -.

REMBL; M3218; AAA32708.1; -.

REMBL; M33218; AAA32708.1; -.

REMBL; M3218; AAA32708.1; -.

REMBL; M318; AAA32708.1; -.

REMBL; M3218; AAA32708.1; -.

REMBC; M3040; AAA3270.1; -.

REMBC; M3040; AAA3270.1; -.

REMBC; M3040; AAA30; 
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S (in Ref. 5).
SD (in Ref. 5 and 7)
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/FIId=CAR 000125.
C -> R (in AMY3).
F -> L (in AMY3).
TT -> DC (in Ref. 5).
C -> T (in Ref. 5).
D -> Y (in Ref. 3).
P -> L (in Ref. 3).
D -> V (in Ref. 3).
I -> L (in Ref. 3).
C -> V (in Ref. 3).
I -> L (in Ref. 3).
D -> H (in Ref. 4).
I -> L (in Ref. 5).
L -> A (in Ref. 5).
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                              PRINTS; PR00110; ÅLPHAAMYLASE.
SMART; SMOG42; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                 InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006604; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
                 MEDLINE=92323146; PubMed=1368777;
                                                                                                                                                                                                                                                                                       EMBL; D10461; BAA01255.1; -. HSSP; P10529; 7TAA.
    SEQUENCE FROM N.A.
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                         Curr. Genet. 17:203-212(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in Oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.; "Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus niger var. awamori.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00642; Aamy, 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
1 21 Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 1; Length 499; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-amylase B.
Nucleophile (By similarity).
Proton donor (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Calcium 2 (By similarity).
By similarity.
By similarity.
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Normaliarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
                                                                                                                                                                                                                                                                                              nassy; Proses; Andrease and cat sub. InterPro; IPR006589; Alp amyl cat sub. InterPro; IPR006047; Alpha amyl cat. InterPro; IPR006046; Glyco hydro 13. Pfam; PF00128; Alpha-amylase; IPRINTS; PR00110; ALPHAAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54921 MW;
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Matches 7; Conservative
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59
185
304
496
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227
231
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ACT_SITE
ACT_SITE
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CARBOHYD
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DISULFID
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similarity).
Calcium 2 (By similarity).
By similarity.
By similarity.
By similarity.
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By lamilarity.
Whinked (GlcMac...) (By similarity).
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
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                                                                                                                     100.0%; Score 40; DB 1; Length 499; 100.0%; Pred. No. 11;
                                                                                                                                                0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Taka-amylase A (EC 3.2.1.1).
                                                                                                                                                                                                                                                                  499 AA
                                                                                                                                  Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                  PRT;
                                                                                            54852 MW;
                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                251
59
185
304
496
218
                                                                                                                                                                                                 162 SSQDYFH 168
                                                                  461
218
499 AA;
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01-DEC-2001 (
01-DEC-2001 (
                         DISULFID
DISULFID
DISULFID
DISULFID
                                                                               CARBOHYD
SEQUENCE
                                                                                                                      Query Match
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Q96TH4
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes; Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. NCBI_TaxID=5070;

Aspergillus shirousami.

25-CT-2004 (Rel. 25, Last sequence update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan Name-AMY;

STANDARD;

AMY ASPSH P30292;

162 SSQDYFH 168

SSQDYFH 7

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Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By

(B

By similarity. Calcium 1 (By similarity). Calcium 1 (via carbonyl oxygen)

similarity)

Alpha-amylase. Nucleophile (By similarity). Proton donor (By similarity).

21 2227 2237 251 318 142 183

us-10-820-200-2_copy_161_167.rup

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"Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in aflatoxin biosynthesis in maize kernels.";
Phytopathology 89:908-914(1999)
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=5059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Lipomycetaceae; Lipomyces.
NCBI_TaxID=34357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 40; DB 2; Length 499; 100.0%; Pred. No. 11; ive 0; Mismatches 0; Indels
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00117;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 45, Last annotation update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0110; ALPHAAMYLASE.
SMART; SMO0642; Aamy; 1.
GLycosidase; Hydrolases
SEQUENCE 499 AA; 54804 MW; BEF42ADA71D20DA9 CRC64;
                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase (EC 3.2.1.1).
                                                                                                                                                           499 AA
                                                                                                                                                           PRT;
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MEDLINE=96132108; PubMed=8593683;
Steyn A.J.C., Pretorius I.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fakhoury A.M., Woloshuk C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                           PRELIMINARY;
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   162 SSQDYFH 168
                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus flavus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=86-10D;
                                                                                                                                                                                                                                                                                                                                                   Name=amy1;
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                                                                                               RESULT 8
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                                                                                                                                                           "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                  Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
Iimura Y.,
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Matsubara T.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

EMBL, ABOSIS15; BADOG02.1; -.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR006047; Alpha amyl cat.

InterPro; IPR006046; Alpha amyl cat.

InterPro; IPR006046; Glyco_hydro_13.

FEAM: PROSE ALPHA ALPHA AMYL SET.

InterPro; IPR006046; Glyco_hydro_13.

FEAM: PROSE ALPHA ALPHA AMYL SET.
                                                                                                                                                                                                                   oryzae.";
Biosci. Biotechnol. Biochem. 64:816-827(2000).
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; ABO21976; BAA95703.1; -.
PIR; JN0588 JN0588.
PIR; S04549; ALAS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 40; DB 2; Length 499; 100.0%; Pred. No. 11; ive 0; Mismatches 0; Indels
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SEQUENCE 499 Aa; 54804 MW; EEF42ADA71D20DA9 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P10529; TTAA.
GO; GO: 0004556; F: alpha-amylase activity; IEA.
GO; GO: 0016798; F: hydrolase activity, acting on
GO; GO: 0005975; P: carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR0066589; Alp amyl_cat.
InterPro; IPR0066689; Alp amyl_cat.
PR006189; Alpha-amylame; I.
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                                                           MEDLINE=20289310; PubMed=10830498;
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499 AA; 54794 MW;
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Q76L99;
05-JUL-2004 (TEMBLEL: 27,
05-JUL-2004 (TEMBLE: 27,
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Matches 7; Conservative
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Name=amyl I;
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SIGNAL
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SMART;

Matches

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Gaps

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311 SSQDYFH 317
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                                                                                 SEQUENCE FROM N.A. STRAIN=KSM 22M;
           NCBI_TaxID=29829;
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05-JUL-2004 (
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Q7RL16
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Q70BE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstain the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Characterization of a novel alpha-amylase from Lipomyces kononenkoae and expression of its gene (LKA1) in Saccharomyces cerevisiae.";
Curr. Genet. 28:526-531(1995).
-!- CATALYIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
!! Linkages in Oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
-!- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
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PIR; JC4510; JC4510.
HSSP; P10529; 7TAA.
InterPro; PR0056047; Alpa amyl_cat_sub.
InterPro; IPR005036; CBM 21.
Pfam; PR01310; CBM 21.
SMART; SM00642; Aamyl_ase; 1.
SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Direct protein sequencing; G1ycoprotein; 1.
28 G1ycoprotein; 1.
28 G1ycoprotein; 1.
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Calcium 2 (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
No similarity.
By similarity.
By similarity.
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Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase.
Alpha-amylase.
Lipomyces starkkeyi.
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales, Lipomycetacese, Lipomyces.
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Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-amylase 1.
Carbohydrate binding type-21.
Nucleophile (By similarity).
Proton donor (By similarity).
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87EB16534F5A9A9F CRC64;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                           "Cloning and expression of Lipomyces starkeyi alpha-amylase in Escherichia coli and determination of some of its properties."; FEMS Microbiol. Lett. 233:53-64 (2004).
EMBL; AYIS5463; AAN75021.1; -.
HSSP; P26877; 1A47.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat_sub.
InterPro; IPR005036; CBM_21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
NOBI_TaxID=323;
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                         Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H., Moon T.-W.,
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Fanelli V., Finetti-Sialer M., Gallitelli D.;

Fanelli V., Finetti-Sialer M., Gallitelli D.;

Fanelli V., Finetti-Sialer M., Gallitelli D.;

Fanelli A.66459; CAE5410.1; --

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008026; F:ATP-dependent helicase activity; IEA.

InterPro; IPR001410; DEAD.

InterPro; IPR001650; Helicase_C.
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Drosophila melanogaster CG11926 gene product, putative
                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00642; Aamy; 1.
SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative helicase.
PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
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Helicase.
SEQUENCE 224 AA; 25431 MW;
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Nature 430:35-44(2004).
EMBL; CR380957; CAG61198.1;
                                                                                                                                                                                                                                                                           6; Conservative
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Matches 6; Conserv
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Coffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boiszame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zzuvanovic I., Bolocin-Pukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii,";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                        PubMed=12368865; DOI=10.1038/nature01099;
Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B., Salzberg S.L., Venter J.C., Waters A.P., Smith H.O., White O.R., Carucci D.J.;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=73239;
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SEQUENCE 596 AA; 69216 MW; 8170C2D33F53117D CRC64;
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EMBL, AABLO1000756, EAA22214.1; -.
InterPro, 1PR004353, Yeast73DUF.
Pfam, PP03164; DUF254; 1.
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                         Name=PY02732;
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EMBL, AF144322, AAD20446.1; -.
InterProy IPR002110, ANK.
Pfam; PF00023; Ank, 3.
PRINTS; PR01415; ANKYRIN.
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"Draft sequence of the diardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.
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Glardia lamblia (Glardia intestinalis).
Eukaryota: Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLP 456 15756 18038.
Glardia lambla ATCC 50803.
Eukaryota: Diplomonadida; Hexamitidae; Giardiinae; Giardia
NCBI_TaxID=184922;
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Pred. No. 1.8e+02;
1; Mismatches 0; Indels
                                                                                                                       Length 627;
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                                                                            627 AA; 71471 MW; DEA0B02466F4F480 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                       Score 36; DB 2;
Pred. No. 92;
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InterPro; IPR002013; Syja N. Pfam; PF02383; Syja N; 1. PROSITE; PS50275; SAC; 1.
                                                                                                                            90.0%;
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Best Local Similarity 85.7;
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| :D475 CRC64; | Query Match 87.5%; Score 35; DB 2; Length 760; Best Local Similarity 85.7%; Pred. No. 1.8e+02; Matches 6; Conservative 1; Mismatches 0; Indels | | |
| SQ SEQUENCE 760 AA; 85542 MW; 12E54841019CD475 CRC64; | Score 35; DB Pred. No. 1.8e ; Mismatches | | |
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Search completed: February 8, 2005, 18:41:55 Job time : 6.10811 secs

Variant a Recombina Sequence

Alpha-amy Variant a

Sequence Sequence

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Streptoco

Bacteria]

Bacillus Wild type Bacillus Bacillus

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Bacillus Bacillus Bacillus Bacillus

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The sequence os that of the Asoergillus oryzae alpha amylase, sold commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergence, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for detergents, dishwashing agents and liquefaction agents.
                                                                                                                                                                                                                                                                                                                              Methionine substitution; stability; activity; detergent; dishwashing agents; liquifaction agents.
                                                                                                                                                                                                    ALIGNMENTS
                 AAR63185
ADS44249
                                  ABP26024
AAR63186
AAR63181
AAR91180
AAR07574
AAR6109
AAP61109
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AAW17594
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92DK-00001503.
93DK-00000292.
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(NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                               Mutant alpha-amylase.
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WO9402597-A1.
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18-JUL-1994
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AAR46065;
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Aar72450 Aspergill
Aar78270 Aspergill
Aaw14500 Aspergill
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Aab84260
Adt89632
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Abb80177
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                               2105692 segs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             US-10-820-200-2_COPY_98_110
                                            OM protein - protein search, using sw model
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AAW14500
ADT89632
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ABP9623
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ABP97834
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AAR88213
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geneseqp2000s:*
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RESULT 2 AAR72450

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Oxidation stable alpha amylases can be used for the simultaneous desizing
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                                                                                                                           Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - for simultaneous desizing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; calcium dependency; substrate binding; stabillty; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction; sweetener; ethanol production; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of an oxidation stable alpha-amylase - for simultaneous des:
bleaching or scouring of fabrics contg. starch or starch derivs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 78; DB 2; Length 478; 100.0%; Pred. No. 0.0011;
                                                                                           Aspergillus oryzae alpha amylase (mature protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pedersen HH,
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                                                                                                                                                                                                                                                                                                                                                  94WO-DK000371.
                                                                                                                                                                                                                                                                                                                                                                                    94DK-00000141.
                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marcher D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-283767/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                               Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                05-0CT-1994;
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                                                       17-JAN-1996
                                                                                                                                                                                                                                                                     WO9521247-A1
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                 AAR78270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, blacching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR-2003 to correct PI field.)
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha amylase, variant, enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Bacillus derived alpha-amylase variants - having amino acid
modifications to improve washing and/or dishwashing performance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bisgard-Frantzen H, Svendsen A, Thellersen M;
                               Score 78; DB 2; Length 478; Pred. No. 0.0011; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 78; DB 2; Length 478; 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus oryzae alpha amylase (mature protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 75-76; 105pp; English.
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                                                                                                                                                                                                                                                     AAR72450 standard; protein; 478
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                                 100.0%;
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94DK-00000140
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(first entry)
                                                                                                                                         78 AYHGYWQQDIYSL 90
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                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus oryzae.
                                                     Local Similarity
les 13; Conserv
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 Sequence 478 AA
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01-DEC-1995
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                                     Query Match
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Gaps

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0; Indels

Aspergillus oryzae

AAR78270 standard; protein; 478 AA.

RESULT 3
AAR78270
ID AAR7

Matches

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fincter an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant Fungamy1; claim 43"

291. 313

/label= loop 8 modification region

/notes art least one amino acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to 322-346 of AAW1498 is deleted or replaced with a
                                                                                                                                                                                                                                                                                                                                           1977. 313

/ Jabel= loop 8 modification region
/ Jabel= loop 8 modification where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 325-345 of AAW1448 is
deleted or replaced with a fragment corresponding to this
fragment; claim 38"
residue of a parent alpha-amylase (used as a template for a variant) corresponding to 196-198 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl—and fungamyl—like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cystein residues in the variant is modified or replaced with a non-proline or non-cystein residue such as alanine. The variants can be used for (dish)washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-amylase variants and methods of production - have altered
properties such as calcium dependency, substrate binding and stability.
                                                                                                                                                                                                                                                                                                                  fragment corresponding to this fragment; claim 36'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 87-88; 171pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                    fragment; claim 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498
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95DK-00001192.
95DK-00001256.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 478 AA;
                                                                                                 Misc-difference
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23-OCT-1995;
10-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9623874-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-1996;
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Matches
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nc 165. 1.77

nc 165. 1.77

nc 165. 1.77

nc 165. 2.77

clast one amino acid residue of a parent alpha force="at least one amino acid residue of a parent alpha emplase (used as a template for a variant) corresponding to 195-202 of AAN14499 is deleted or replaced with a fragment corresponding to this fragment; claim 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /labels loop 2 modification region
/notes "at least one amino acid residue of a parent alpha
amylase (used as a template for a variant) corresponding
to 44-57 of AAM14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
amylase (used as a template for a variant) corresponding
to 117-185 of AMM4499 is deleted or replaced with a
fragment corresponding to this fragment; claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 121-181 of AAW14499 is deleted or replaced with a fragment corresponding to this
                         /label= loop 1 modification region
/label= nat least one amino acid residue of a parent alpha
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 7-23 of AAW14499 is deleted or replaced with a
                                                                                                                                                                                                                                                                                                                                                                  /label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
amylase (used as template for a variant) corresponding
to 12-19 of AAM 4499 is deleted or replaced with a
fragment corresponding to this fragment; claim 30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "at least one amino acid residue of a pareht alpha amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding 48-51 of AAM14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylabee (used as a template for
a variant) corresponding to 14-15 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                      /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template fa a variant) corresponding to 8-18 of AAW1499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "preferred region where at least one amino acid
                                                                                                                                              fragment corresponding to this fragment; claim 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= loop 2 modification region
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/label= loop 3 modification region
                                                                                                                                                                                            label= loop 1 modification region
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                                                                                                                                                                                                                                                                                                                  fragment; claim 35"
     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eragment; claim 20"
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/label= lo
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     Key
Misc-difference
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Gaps

Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological

(NOVO) NOVOZYMES BIOTECH INC.

Brody H;

Connelly M,

WPI; 2004-708545/69.

N-PSDB; ADT89631

31-MAR-2004; 2004US-00815495. 31-MAR-2003; 2003US-0459902P. Example 11; SEQ ID NO 22; 58pp; English.

substance

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The present sequence represents a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, conspecification describes variants of this fungamyl-like alpha-amylase, which have an alteration in one the amino acid regions 98-110, 150-160, 150-160, 151-167, 280-288, 448-455, and 468-475. Bach alteration is a deletion or substitution of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic pH, relative to wild-type enzyme. The variants can therefore be used at higher conversion or faster reaction, and have reduced need for cooling and reduced risk of contamination). The variants may also be used in conjunction with other enzymes, particularly of may also be used uning dextrinisation. The variants are used to produce syrups, particularly of high maltose content, or alcohol, from starch; as dough improver for baked goods; in the variant, to increase fermentability of the wort; and for liquefaction of starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variant of Fungamyl-like alpha-amylase, useful for production of maltose syrups, includes mutations that improve stability against heat and acidic pH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                    Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose; alcohol; starch; dough improver; brewing; starch liquification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus niger neutral alpha-amylase A (amyA) protein.
Amino acid sequence of a fungamyl-like alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glucoamylase; glaA; amyA; alpha-amylase A; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pedersen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 42-45; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADT89632 standard; protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                             10-NOV-2000; 2000WO-DK000626
                                                                                                                                                                                                                                                                                                                                                                        99DK-00001617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 AYHGYWQQDIYSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-367478/38.
N-PSDB; AAF90208.
                                                                                                                                         Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 498 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004191864-A1
                                                                                                                                                                                                 WO200134784-A1
                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1999;
                                                                                                                                                                                                                                                        17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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11D ADT8

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                                                                                                                                                                                                                                    The present invention relates to a method of producing heterologous halological substance. The method involves culturing mutant of wild-type happergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance and second nucleotide heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus niger neutral alpha-amylase B (amyB) protein.
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 78; DB 8; 100.0%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT89628 standard; protein; 499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVOZYMES BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2003; 2003US-0459902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2004; 2004US-00815495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYHGYWQQDIYSL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-708545/69.
N-PSDB; ADT89627.
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 13, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                            Sequence 498 AA;
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ADT89628
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Gaps

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The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose isomerase, or glucoamylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act upon the desired substrate. Also described are self-processing transgenic upon the desired substrate, and escribed are self-processing transgenic processing. Also described is a method (M) for converting starch to starch-derived products in a transformed plant part, (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful for preparing maltodextrin. A transformed plant (TP) can be used to produce food products having improved taste and to produce fermentable
          The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Craig J, Kinkema M;
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                                                                                                                                                                                                                            100.0%; Score 78; DB 8; Length 499; 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP96630 standard; protein; 1095 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Batie CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2001; 2001US-0315281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2002; 2002WO-US027129
                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 107; 158pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                        1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                    13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus shirousami
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-268420/26.
                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                          Sequence 499 AA;
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                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                    Matches
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The sequences given in ABB80164-87 show enzymatic proteins derived from A. funigatus. These proteins display the catalytic activity of an enzyme such as tannase, callulase, glucose oxidase, glucoamylase, phytase, betaglactosidases, invertase, lipase, alpha-amylase, laccase, polygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of compositions comprising the tannase are useful for modulating the amount of cellulose in a composition. Compositions comprising the amount of cellulose in a composition comprising the amount of glucose or oxygen in a composition. Compositions comprising phytase are useful for modulating the amount of myo-inosicol phosphates in a composition. Composition comprising comprising the amount of myo-inosicol phosphates in a composition of lactose in a composition com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase; beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodaxtrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability.
(M) eliminates the need
                        to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents alpha-amylase/glucoamylase fusion protein, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                               Gaps
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feed,
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                                                                                                                                                                                                           Length 1095;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                        100.0%; Score 78; DB 6; Le
100.0%; Pred. No. 0.0025;
  substrates for ethanol and fermented beverages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bussey H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 134-35; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80177 standard; protein; 495 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-AUG-2002; 2002WO-US024842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                      1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                       13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-332729/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. fumigatus AfAAL1
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                               Sequence 1095 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003012071-A2
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                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                     Matches
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modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising laccase are useful for modulating the amount of oxidated phenolic compounds in a composition. Composition comprising polygalacturonases are useful for modulating the amount of Nylan or xylo-oligomers polygalacturonic acid chains in a composition. Composition comprising cylogalacturonic acid chains in a composition. Composition and corresponding DNA's are useful in various industries such as those involved in the masking of food and feed, beverages, textiles and detergants. The DNA's are useful to express recombinant enzymes for characterization, modification or compares vith the nucleotide sequence of A.fumigatus to identify duplicated genes of paralogs having the same or similar blochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify potential orthologous enzyme genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, and to raise anti-protein antibodies. The polypeptide having cannows the colour, flavour and health benefite of tea products, improves the colour, lavour and health benefite of tea products, cativity enhances cleaning ability of detergent compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 6; Length 495;
Pred. No. 0.0032;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae TAKA protein (TAA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 188; 196pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB09072 standard; protein; 423 AA.
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(SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 AYHGYWQQDIYSV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AYHGYWQQDIYSL 13
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KR2001027418-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB09072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abboog Ab
              %XGGGGGGGGGGGGGGGGGGGGGGGG
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The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic

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amytace. Maintacturing marticle amytace completes. The following a construct of the constru
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всерв:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosidic linkage; oligosaccharide; polysaccharide; baking.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide from a filamentous fungus, preferably Aspergillus niger, useful in a baking process.
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amylase. Manufacturing maltogenic amylase comprises the following
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of an alpha-amylase of Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 4; Length 423; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Albermann K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Folkers U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 61-63; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP97894 standard; protein; 494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wagner C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.7%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2001; 2001EP-00000380.
16-AUG-2001; 2001EP-00000381.
16-AUG-2001; 2001EP-00000382.
16-AUG-2001; 2001EP-00000383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2002; 2002WO-NL000522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-2001; 2001EP-00000379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2001; 2001EP-00000384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in a baking process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 AMHGYWQODIYSL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stock A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003016535-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAM ) DSM NV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maier D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP97894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562) stockated from a T. lanuginosus gene library. The recombinant enzyme (54-60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7 and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                   Thermophilic alpha-amylase with activity range of 60-80 degrees C -derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs and bakery prods. esp. bread.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; heat behindels; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                           Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69; DB 2; Length 493;
Pred. No. 0.027;
3; Mismatches 0; Indels
                                                                                                                                      1. .18
/label= Sig_peptide
                                                                                           Thermomyces lanuginosus; CBS 224.63
                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 36-38; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS23436 standard; protein; 500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                           Rasmussen
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                                                                                                                                                                                                                                                                                                           (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT10562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003233675-A1
                              Alpha-amylase
                                                                                                                                                                                                                                                                             04-JUL-1994;
                                                                                                                                                                                                                                                                                                                                          Michelsen B,
                                                                                                                                                                                                                                                03-JUL-1995;
                                                                                                                                                                                     WO9601323-A1
 03-APR-1996
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                                                                                                                                                                                                                   18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADS23436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          field)
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Matches
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                                                                                                                                                                                                                                                                                                                                                        enzyme; baking; Thermomyces lanuginosus; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermophilic alpha-amylase with activity range of 60-80 degrees C -derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragments (AAR88213-14) of Thermomyces lanuginosus thermostable alpha-
amylase (AAR88212) are the products of DNA fragments (AAT10565-66)
generated from T. lanuginosus genomic DNA by PCR using primers based on
conserved regions of alpha-amylase genes. (Updated on 16-OCT-2003 to
standardise OS field)
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                            Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 2; Length 55;
Pred. No. 0.0027;
3; Mismatches 0; Indels
                                                                           1; Indels
                                           Score 70; DB 6;
Pred. No. 0.019;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Thermomyces lanuginosus; CBS 223.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 40; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR88212 standard; protein; 493 AA.
                                                                                                                                                                                                                 AAR88213 standard; peptide; 55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and bakery prods. esp. bread.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.5%;
76.9%;
                                            89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-EP002607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94GB-00013419
                                                                                                                                                                                                                                                                                                                                                        Alpha-amylase; thermostable polymerase chain reaction.
                           Query Match
Best Local Similarity 84.0%,
Best Local 11; Conservative
                                                                                                                         Michelsen B, Rasmussen P;
                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                        1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 76.2
Best Local 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||||:|:|||
26 SYHGYWQKDLYSL 38
                                                                                                                                                                                                                                                                                                                           Alpha-amylase fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2003 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-087673/09.
N-PSDB; AAT10565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DANI-) DANISCO AS
              Sequence 494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9601323-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-1995;
                                                                                                                                                                                                                                                                           16-OCT-2003
03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-1996
                                                                                                                                                                                                                                              AAR88213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR88212
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RESULT 13
AAR88212
ID AAR88
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AC AAR88
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DT 16-OC

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynuclectide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as major construct and growing the transformed plant where the catecombinant DNA construct and growing the transformed plant where the polynuclectide or polypeptide is useful for improving plant with the compinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with construct is useful for of increased plant, where the polynuclectide or polypeptide is useful for of ingroved plant properties. Configuration of acconditions, pathogens or pease, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rate by modification of content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lighin production or improved allows when the properties or providing improved lighin production or improved allows when the properties or producing the producing contains and produced produced to the producing or provided the producing or producing the producing or producing the producing plant growth and development under at least one stress condition, majored produced produce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 0.027;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen X, Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 12469; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN19570 standard; protein; 513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao Y, Hinkle GJ, Slater SC,
                                                                              20-FEB-2003; 2003US-00369493
                                                                                                                                                            21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial polypeptide #2223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-2004 (first entry)
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82 AYHGYWAQDMYSL 94
                                                                                                                                                                                                                                      CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                  (GOLD/) GOLDMAN B S.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprised by a migroved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the copymolectide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant with the improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme commolic conditions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of content, improved yield by modification of carbohydrate, nitrogen or content, improved yield by modification of carbohydrate, nitrogen or providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form from the form ispan or the form at the printed specification but was obtained in electronic form and the mispan of the day of the d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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bacterial polypeptide.
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Pred. No. 0.057;
2; Mismatches 1; Indels
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Job time : 7.787 secs
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-182-859-7
US-09-656B-2
US-08-40-7702-6
US-08-40-7702-6
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| 6555 6555 6555 6555 6655 6683 6683 7125 7125 7425 7425 7425 7425 7425 7425 7425 74 | T 1 -720-899-7 uence 7, Application US/0872 ent No. 573460 MERAL INFORMATION: APPLICANT: Bisgaard-Frantze APPLICANT: Borchert, Torben APPLICANT: Borchert, Torben APPLICANT: Yend der Zee, Pia TITLE OF INVENTION: AMYLASE MUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 57534600 No. STREET: 405 Lexington Ave CITY: New York COUNTRY: NEADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 104 PC COMPATION APPLICATION NUMBER: US/08 FILING DATE: 10-OCT-1996 CLASSIFICATION NUMBER: US/08 FILING DATE: 10-OCT-1996 CLASSIFICATION NUMBER: 31,2 REFERENCE/DOCKET NUMBER: TELEFAX: 21-867-0123 TELECOMMUNICATION INFORMATION: RAPER STRANTON NUMBER: 31,2 TELEFAX: 21-867-0123 TELEFAX: 21-867-0123 TELEFAX: 21-867-0123 TELEFAX: 21-867-0123 TELECOMMUNICATION INFORMATION: RAPER STRANTON ROR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: TYPE: anino acids | i a |
| | cation cation: sgaard- sgaard- sgaard- relleren mider Z TILON: TI | inear rity nserv |
| 00000000000000000000000000000000000000 | T 1 -720-899-7 uence 7, Application ent No. 5733460 MERAL INCORMATI APPLICANT: Bisgaard- APPLICANT: Borchert, APPLICANT: Svendsen, APPLICANT: Thellerse APPLICANT: You der Z TITLE OF INVENTION: WUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: No. 575 STREET: 405 Lexing CITY: New York COUNTRY: 104-6401 COMPUTER: EBADBLE FOR MEDIUM TYPE: Flopp COMPUTER: 100-CC CLASSIFICATION NUMBER: FILING DATE: 22-NO ATTORNEY/AGENT INFORM NAME: LOWNEY DE:, REFERENCE/DOCKET NU TELEFAX: 212-867 TELECOMMUNICATION INF TELEFAX: 212-867 TELEFAX: 212-867 TELECOMMUNICATION INF TELEFAX: 212-867 TELEFAX: 212-867 TELECOMMUNICATION INF TELEFAX: 212-867 TELECOMMUNICATION INF TELEFAX: 212-867 TELECOMMUNICATION INF TELEFAX: 212-867 TELEFAX: | LOGY: linear 99-7 ch 1 Similarity 13; Conserv |
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| | RESULT Sequence of the sequenc | ; US-08 Que Bes Mat |
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CURKESPUNDENCE ADURKES:

OUNDESCEE: No. 5989169disk of No. 5989169th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: 13-FBB-1996
CLASSIFICATION NUMBER: 13-FBB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: No. 58308370 No. 5830837disk of No. 5830837th America, Inc.
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: PatentIn Pelease #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/343,804

FILING DATE: 22-NOV-1994

CLASSIFICATION NUMBER: 31.274

REGISTRATION NUMBER: 31.274

RELEPHONE: 212-867-0123

TELEFRAK: 212-867-0123

TELEFRAK: 212-867-0123
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                     405 Lexington Avenue, 64th Floor
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APPLICANT: Svendsen, Allan
APPLICANT: Bigg rd Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Borchert, Torben Vedel
APPLICANT: SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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STRANDEDNESS: sir
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                                  New York
New York
                                                                       COUNTRY:
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Patent No. 5830837

GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Gaps

us-10-820-200-2_copy_98_110.rai

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RESULT 7
US-09-672-459-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADRESS:
ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STREET: New York
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                    100.0%; Score 78; DB 2; Length 478; 100.0%; Pred. No. 0.00012; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08683838A Patent No. 6022724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acide
TYPE: amino acid
STRANEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                      78 AYHGYWQQDIYSL 90
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                        1 AYHGYWQQDIYSL 13
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-683-838A-10
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US-08-683-838A-10
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RESULT 6 US-09-182-859-7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 78; DB 3; Length 478; 100.0%; Pred. No. 0.00012; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROGREAL INCORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torban
APPLICANT: Borchert, Torban
APPLICANT: Borchert, Torban
ITTLE OF INVENTION: Alpha-Amylase Mutants
ITTLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: 09/82,859
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 0515/96
PRIOR APPLICATION NUMBER: 0712/96
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR PILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 0775/96
PRIOR APPLICATION NUMBER: 1263/96
PRIOR 
Sequence 7, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Blagard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204 US
CURRENT FILING DATE: 1996-10-29
CURRENT FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-07-11
SARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
SARLIER FILING DATE: 1996-07-11
SARLIER FILING DATE: 1996-07-11
SARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
SOFTWARE: FABSCE for Windows Version 3.0
SOFTWARE: FABSCE for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09672459
Patent No. 6436888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AYHGYWQQDIYSL 13
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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Variant-Type Carbohydrate Hydrolase,
Variant Gene Of The Enzyme And Method For Producing
Oligosaccharide Using The Enzyme
is Sequence 2, Application US/08339715A
; Sequence 2, Application US/08339715A
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
APPLICANT: Kanaka, Hiroki
APPLICANT: Shimada, Jiro
APPLICANT: Takata, Hiroki
APPLICANT: Takata, Hiroki
APPLICANT: Takata, Hiroki
APPLICANT: Oranse, Michiyo
APPLICANT: Oranga, Shigetaka
TITLE OF INVENTION: NEOPULLULANASE
NUMBER OF SEQUENCES:
TITLE OF INVENTION: NEOPULLULANASE
NUMBER OF SEQUENCES:
ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
STREET: Metropolitan Square Building, Suite 800, 1450
STREET: Washington
STREET: D.C.
COUNTRY: USA
ZIP: 2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; DB 2; Length 478;
Pred. No. 0.044;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,715A
FILING DATE: 14-NOV-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UP 306096/1993
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Melser, Allen S.
REGISTRATION NUMBER: 27,215
REGISTRATION NUMBER: 27,215
REGISTRATION NUMBER: 27,215
REGISTRATION NUMBER: 27,215
REGISTRATION NUMBER: 202-824-8000
TELLEPAK: 202-824-8000
TELLEPAK: 202-824-8199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-715A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.5%;
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TELEX: 248516
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AYHGYWQQDIYSL 13
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Best Local Similarity 84.6
Matches 11, Conservative
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                                                                                      Sequence 10, Application US/09636252A

Sequence 10, Application US/09636252A

Patent No. 6440716

GENERAL INFORMATION:
APPLICANT: Stenden, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
TTILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2

CURRENT FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: 08/09/636,252A

CURRENT FILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 16

SOFFWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 10

LENDER: APPLICATION NUMBER: 08/09/07-18

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 10

LENDER: APPLICATION NUMBER: 08/09/07-18

SEQ ID NO 10

LENDER: APPLICATION NUMBER: 08/09/07-18

MUTABER OF SEQ ID NOS: 16

SEQ ID NO 10

LENDER: APPLICATION NUMBER: 08/09/07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRUERCE 7, Application US/10186042
| Patent No. 6642044
| GRNERAL INFORMATION:
| APPLICANT: Svendsen, Allan
| APPLICANT: Borchert, Torben
| APPLICANT: Busgard-Frantzen, Henrik
| APPLICANT: Blosgard-Frantzen, Henrik
| FILE REFERENCE: 4796.204-US
| CURRENT APPLICATION NUMBER: US/10/186,042
| CURRENT APPLICATION NUMBER: US/09/672,459
| PRIOR APPLICATION NUMBER: US/09/672,459
| PRIOR PILING DATE: 1900-09-28
| PRIOR PILING DATE: 1900-09-28
| PRIOR PILING DATE: 1996-10-29
| PRIOR PILING DATE: 1996-07-29
| PRIOR PILING DATE: 1996-04-30
| PRIOR PILING DATE: 1996-04-30
| PRIOR PILING DATE: 1996-07-11
| PRIOR PILING DATE: 1996-11-08
| NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AYHGYWQQDIYSL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: A. oryzae
US-09-636-252A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 478
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Gaps

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APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOLCHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 54; DB 1; Length 468; 53.8%; Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARE: 32,181
REFERENCE/DOCKET NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 33,181
TELEROMMULICATION INFORMATION:
TELEROMMULICATION INFORMATION:
TELEROMMULICATION INFORMATION:
TELEROMMULICATION INFORMATION:
TELEBRAKE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church STATE: Virginia COUNTRY: U.S.A. ZIP: 22042 COMPUTRY READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTR: IBM PC compatible COMPUTR: IBM PC C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08467831
Patent No. 5635378
GENERAL INFORMATION:
   FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC 3.2,181
REFERENCE/DOCKET NUMBER: 234-.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELERAX: (703) 205-8050
TELERAX: (703) 205-8050
TELERAX: 248345
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248345
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||:| ::|| :
79 AYHGFWMKNIYKI 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
US-08-470-702-6
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US-08-467-831-6
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Patent No. 5631149

GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: MININI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE BIrch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatchbouse Road, Suite 500 East
CITY: Falls Church
STREET: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION NUMBER: US/08/204,656B
FILING DATE: O2-MAR-1994
CLASSIFICATION NUMBER: 33,181
REFERENCE/DOCKET NUMBER: 33,181
REFERENCE/DOCKET NUMBER: 33,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEBRONE: (703) 205-8050
TELERAX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITES:: 0110 Garchouse Road, Sulte 500 East.
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: R.POPDY disk
COMPUTER: P.C.OMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 1
Pred. No. 0.82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (702,
TELEFAX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER STICS:
LENGTH: 468 amino acids
"VOE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.8%
The Conservative
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79 AYHGFWMKNIYKI 91
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US-08-470-702-6
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Patent No. 5631149
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08204656B
Patent No. 553882
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matsui, Ikuo
APPLICANT: Mishit, Sachio
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                      Gaps
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                                                                                                                                                  Score 54; DB 1; Length 468; Pred. No. 0.82;
                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FLING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/POCKET UNBER: 32,181
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELEFRA: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Birch, Stewart, Kolasch & Birch, LLP
T: 8110 Gatehouse Road, Suite 500 East
Falls Church
Virginia
                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                     69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AYHGYWQQDIYSL 13
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79 AYHGFWMKNIYKI 91
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79 AYHGWWMKNIYKI 91
                                                                                                                                                                                                   7; Conservative
                  TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Falls Churc
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                      ; ANTI-SENSE: NO US-08-467-831-6
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RESULT 15 US-08-470-702-7 . Sequence 7, Application US/08470702

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APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1.2;
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                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PPC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 33,181
REFERENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8050
TELEPRA: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 1
Pred. No. 1.2;
4; Mismatches
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Job time : 2.67439 secs
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.9
Best Local Similarity 53.8
Matches 7; Conservative
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79 AYHGWWMKNIYKI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                        CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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Sequence Sequence Sequence Sequence Sequence

Sequence 22679, A Sequence 108, Appl Sequence 108, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 206, Appl Sequence 2, Appl Sequence 196, Appl Sequence 196, Appl Sequence 3, Appl Sequence 598, Appl Sequence 459, Appl Sequence 45

US-10-369-493-22723 US-10-369-493-22679 US-10-10-18-19-44 US-10-18-19-18-10-18 US-10-369-493-597 US-10-369-493-597 US-10-369-493-15914 US-10-369-493-15914 US-10-369-493-15914 US-10-369-493-15914 US-10-388-305-206 US-10-388-305-206 US-10-388-305-206 US-10-388-305-196 US-10-388-305-196 US-10-369-493-23599 US-10-369-493-23599 US-10-14-436-3 US-10-14-436-3 US-09-978-459-459 US-09-978-459-459

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1. (cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

1. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

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2. (cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

3. (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1373511
                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1373511 segs, 325702437 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                US-10-820-200-2_COPY_98_110
78
                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                         1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                           8,
                                                     Copyright
                                                                                                                                                                                                           February
                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                           Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | | SUMMARIES | | | |
|--------|-------|-------|--------|----|---------------------|-------------|-------------------|--|
| Result | | Query | Query | | | | | |
| No. | Score | Match | Length | DB | ID | Description | uo | |
| 1 | 7.8 | 100.0 | 478 | 14 | US-10-184-771-10 | Seguenc | e 10, Appl | |
| ~ | 78 | 100.0 | 478 | 14 | US-10-186-042-7 | Sequenc | e 7, Appli | |
| m | 78 | 100.0 | | 15 | US-10-644-187-7 | Sequenc | Sequence 7, Appli | |
| 4 | 78 | 100.0 | | 11 | US-10-926-720-10 | Seguenc | e 10, Appl | |
| S | 78 | 100.0 | 498 | 16 | US-10-815-495-22 | Sequence | e 22, Appl | |
| 9 | 78 | 100.0 | | 16 | US-10-815-495-18 | Seguence | | |
| 7 | 78 | 100.0 | _ | 14 | US-10-228-063-45 | Sequence | | |
| 80 | 75 | 96.2 | | 14 | US-10-213-990-42 | Sequence | | |
| σ | 69 | 88.5 | | 15 | US-10-369-493-12469 | Sequence | | |
| 10 | 67 | 85.9 | | 15 | US-10-369-493-2223 | Sequence | e 2223, Ap | |
| 11 | 65 | 83.3 | | 14 | US-10-213-990-48 | Sequence | e 48, Appl | |
| 12 | 64 | 82.1 | | 15 | US-10-416-393-1 | Sequence | | |
| 13 | 58 | 74.4 | | 14 | US-10-213-990-45 | Sequence | e 45, Appl | |

| | | Length 478; Indels 0; Gaps 0; | |
|------------|--|---|--|
| ALIGNMENTS | RESULT 1 US-10-184-771-10 i Sequence 10, Application US/10184771 i Publication No. US20030170769A1 i GENERAL INFORMATION: i APPLICANT: Svendeen, Allan i APPLICANT: Bisgard-Frantzen, Henrik i APPLICANT: Borchert, Torben Vedel ITILE OF INVENTION: Alpha-Amylase Mutants i FILE REFERENCE: 0776/1F216-US2 CURRENT FILING DATE: 2002-06-28 FRIOR RPLICATION NUMBER: US/09/636,252 i CURRENT FILING DATE: 2000-08-10 i PRIOR PILING DATE: 2000-08-10 i PRIOR FILING DATE: 1996-07-18 i NUMBER OF SEQ ID NOS: 16 i SOFTWARE: FastesEQ for Windows Version 3.0 i LENGTH: 478 i CREATER: A OFYZAE US-10-184-771-10 | Query Match 100.0%; Score 78; DB 14; Best Local Similarity 100.0%; Pred. No. 0.00087; Matches 13; Conservative 0; Mismatches 0; Qy 1 AYHGYWQQDIYSL 13 | RESULT 2 US-10-186-042-7 ; Sequence 7, Application US/10186042 |

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RESULT 5
US-10-815-495-22
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100.0%; Pred. No. 0.00087;
ive 0; Mismatches 0; Indels
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| Conservation No. US20040048351A1
| CONERAL INFORMATION |
| CONERAL INFORMATION |
| APPLICANT: Svendean, Allan |
| APPLICANT: Bisgard-Frantzen, Henrik |
| TITLE OF INVENTION: Alpha-Amylase Mutants |
| FILE REPERBNGE: 4796.204-US |
| CURRENT APPLICATION NUMBER: US/10/644,187 |
| CURRENT FILING DATE: 2003-08-20 |
| PRIOR FILING DATE: 1998-10-29 |
| PRIOR FILING DATE: 1996-04-30 |
| PRIOR FILING DATE: 1996-04-30 |
| PRIOR FILING DATE: 1996-06-28 |
| PRIOR FILING DATE: 1996-07-11 |
| PRIOR FILING DATE: 1996-11-08 |
| NUMBER OF SEQ ID NOS: 37 |
| CONTAMARE: FASTSEQ FOR WINDOWS VERSION 3.0 |
| CONTAMARE |
| C
                                                                          GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert Torben
APPLICANT: Borchert Torben
APPLICANT: Borchert Torben
APPLICANT: Bagard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REPERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
FRIOR APPLICATION NUMBER: US/09/672,459
FRIOR APPLICATION NUMBER: 09/182,859
FRIOR FILING DATE: 1908-10-29
FRIOR FILING DATE: 1996-06-28
FRIOR FILING DATE: 1996-07-11
FRIOR APPLICATION NUMBER: 0715/96
FRIOR FILING DATE: 1996-07-11
FRIOR APPLICATION NUMBER: 1263/96
FRIOR FILING DATE: 1996-07-11
FRIOR APPLICATION NUMBER: 1263/96
FRIOR FILING DATE: 1996-11-08
FRIOR FILING DATE: 1996-11-08
FRIOR FILING DATE: 1996-11-08
FRIOR FILING DATE: 1996-11-08
FRIOR APPLICATION NUMBER: 1263/96
FRIOR FILING DATE: 1996-11-08
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FRIOR APPLICATION NUMBER: 1263/96
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FRIOR APPLICATION NUMBER: 1263/96
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FRIOR FILING DATE: 1996-11-08
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FRIOR FILING DATE: 1996-11-08
FRIOR APPLICATION NUMBER: 1263/96
FRIOR FILING DATE: 1996-11-08
FRIOR FILING DATE: 1996-11-08
FRIOR APPLICATION NUMBER: 1263/96
FRIOR FILING DATE: 1996-11-08
FRIOR FILING DATE: 1996-11-08
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Publication No. US20030171236A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 13; Conservative
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US-10-644-187-7
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Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION UNDERE: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/926,720
FILING DATE: 26-Aug-2004
CLASSIFICATION: UNKNOWN>
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                                                                                                                                                                                                                                                        ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REGISTRATION NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-87-055
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                             APPLICANT: Svendsen, Allan
Bisg+rd-Frantzen, Henrik
Borchert, Torben Vedel
TITLE OF INVENTION: -Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US/2050019886A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 478 amino acids
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Matches 13; Conserva
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Gaps

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Indels

1 AYHGYWQQDIYSL 13

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Sequence 12469, Application US/10369493
; Publication No. US2030233675A1
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
; APPLICANT: Blater, Steven C.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)8
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12469
                                          Sequence 42, Application US/10213990

Sequence 42, Application No. US20030082595A1

Bublication No. US20030082595A1

GENERAL INFORMATION:

APPLICANT: Ususey, Howard

APPLICANT: Storms, Reg

APPLICANT: Storms, Reg

APPLICANT: Storms, Reg

TITLE OF INVENTION: ENZYMES AND METHODS OF USE

TITLE OF INVENTION: ENZYMES AND METHODS OF USE

TITLE OF INVENTION: UNDER: 10182-019-999

CURRENT FILING DATE: 2002-08-05

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PASLESEQ for Windows Version 4.0

SEQ ID NO 42

LENGTH: 495
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Pred. No. 0.0026;
1; Mismatches 0; Indels
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84.6%; Pred. No. 0.021;
tive 1; Mismatches 1; Indels
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: HINK-b, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-12469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AYHGYWQQDIYSV 109
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 84.6
Matches 11; Conservative
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ORGANISM: Aspergillus
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US-10-369-493-12469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-10-369-493-2223
                                   US-10-213-990-42
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US-10-815-495-18

US-10-815-495-18

Sequence 18, Application US/10815495

Publication No. US20040191864A1

GENERAL INFORMATION:

APPLICANT: Novozymes Biotech, Inc.

APPLICANT: Connelly, Mariah

APPLICANT: Brody, Howard

TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient

TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient

TITLE OF INVENTION: Methods For Producing Biological

TITLE OF INVENTION INVENTION FOR PRODUCE

TITLE OF INVENTION FOR PRODUCE

TITLE 
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; Sequence 45, Application US/10228063
; Sequence 45, Application WS/10228063
; Publication Wo. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Salf-processing Plants and Plant Parts
; TITLE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER: FSEQ ID NOS: 60
; SOFTWARE: FSECSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 78; DB 16; Length 499; Best Local Similarity 100.0%; Pred. No. 0.0009; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         Length 498;
                                                                                                                                                                                                                                                                                                             0; Indels
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100.0%; Score 78; DB 16;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 13; Conservative 0; Mismatches 0;
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US-10-228-063-45
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                       99 AYHGYWQQDIYSL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18
                                                                                                   ; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 AYHGYWQQDIYSL 111
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) NAME/KEY: misc feature
; OTHER INFORMATION: SEQ ID NO:1
US-10-416-393-1
                                                                                                                                                                                                                                   78 AYHGYWQQKIYDV 90
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                                                                                                     Query Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                              1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 61.5
Matches 8; Conservative
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ORGANISM: Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-369-493-22723
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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT PILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
LENGTH: 513
LENGTH: 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/10213990
Fublication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Roemer, Terry
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FRRENCE FREE OF WINDOWS Version 4.0
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| Publication No. US20040091983A1 |
| Publication No. US20040091983A1 |
| GENERAL INFORMATION: |
| APPLICANT: Veit, Cristopher |
| APPLICANT: Felby, Claus |
| TITLE OF INVENTION: SECONBRY LIQUEFACTION IN ETHANOL PRODUCTION |
| FILE REFERENCE: 10113.204-US |
| CURRENT APPLICATION NUMBER: US/10/416,393 |
| CURRENT FILING DATE: 2003-10-14 |
| NUMBER OF SEQ ID NOS: 1 |
| SEQ ID NO 1 |
| SEQ ID NO 1 |
| LENGTH: 484 |
| TYPE: PRT |
| ORGANISM: Aspergillus niger |
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Pred. No. 0.044;
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Pred. No. 0.095;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2223
                                                                                                                                                                                                                                                                                                                       85.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 83.3%;
1 Similarity 76.9%;
10; Conservative
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103 AYHGYWVQDMYAL 115
                                                                                                                                                                                                                                                                                                                                                                                                          1 AYHGYWQQDIYSL 13
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 48
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-48
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Best Local Similarity
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: BAPPLICATION WUMBER: US/10/369,493
CURRENT PEPLING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-29
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22723
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Sussey, Howard
APPLICANT: Scomer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 630
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  DB 15; Length 484;
                                                      2; Indels
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ORGANISM: Schizosaccharomyces pombe
FEATURE:
NAME/KEY: unsure
1. CCATION: (1)...(493)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-22723
Score 64; DB 1:
Pred. No. 0.12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 22723, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                   US-10-213-990-45

"Sequence 45, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
     82.1%;
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101 SYHGYWQQNIHEV 113
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RESULT 15
US-10-369-433-22679
i Sequence 22679, Application US/10369493
j Fublication No. US20030233675A1
j Fublication No. US20030233675A1
j GENERAL INFORMATION:
j APPLICANT: Care y Yongwei
j APPLICANT: Slater, Steven C.
j APPLICANT: Goldman, Barry S.
j APPLICANT: Chen, Xianfeng
j TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
j TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
j FILE REFERENCE: 38-10 (52052) B
j CURRENT APPLICATION NUMBER: US 10/369, 493
j CURRENT APPLICATION NUMBER: US 60/360, 039
j PRIOR FILING DATE: 2002-02-21
j PRIOR FILING DATE: 2002-02-21
j SEQ ID NOS: 47374
j SEQ ID NO 22679
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Query Match 71.8%; Score 56; DB 15; Length 493; Best Local Similarity 69.2%; Pred. No. 2; Matches 9; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.9%; Score 53; DB 15; Length 564; Best Local Similarity 69.2%; Pred. No. 6.6; Matches 9; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 8, 2005, 19:05:53 Job time : 6.92986 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; CRGANISM: Schizosaccharomyces pombe US-10-369-493-22679
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100 AYHGYWNTDYESL 112
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89 AYHGYWAQDMTQL 101
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                                                                                               1 AYHGYWQQDIYSL 13
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

    protein search, using sw model
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OM protein

February Run on:

8, 2005, 18:28:34; Search time 1.50579 Seconds (without alignments) 830.671 Million cell updates/sec

US-10-820-200-2_COPY_98_110

1 AYHGYWQQDIYSL 13 score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

alpha-amylabe (EC alpha-amylabe (EC alpha-amylase (EC pullulanase (EC 3 alpha-amylase (EC 3 alpha-amylase (EC probable alpha-amy probable alpha-amy alpha-amylase (EC probable alpha-amylase) alpha-amylase (EC alpha-amylase VCA0 alpha-amylase - fi alpha-amylase (EC cyclomaltodextrin cyclomaltodextrin cyclomaltodextrin cyclomaltodextrin alpha-amylase (EC alpha-amylase Description SUMMARIES ALAS1 ALAS3 JS0663 JT0466 JN0588 B48305 JACC201 JCC4510 S31478 ALBYAF ALBYAF T38448 T41503 S62505 S62505 S06115 T41603 ALBSK ALBSK ALBSK S72270 A35282 S33921 ALBSXR A58800 A48305 DB Query Match Length 100.0 67.9 66.7 64.1 64.1 62.3 Score Result

| cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | glycosyl hydrolase | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | alpha-amylase (EC | alpha-amylase (EC | alpha-amylase (imp | alpha-amylase (imp | _ |
|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------|
| 809196 | ALBSG6 | ALBSGC | ALBSMX | G75392 | ALKBG | ALBSX1 | 139805 | 863598 | ALBSXF | ALBSGR | S28784 | AH0979 | F91185 | D86032 | S23807 |
| ~ | - | - | - | 8 | H | | N | N | H | - | н | ~ | N | ~ | 7 |
| 713 | 718 | 718 | 718 | 483 | 655 | 703 | 704 | 710 | 711 | 714 | 717 | 675 | 919 | 949 | 9/9 |
| 80 | 2.8 | 62.8 | 62.8 | 60.3 | 60.3 | 59.0 | 59.0 | 59.0 | 59.0 | 59.0 | 57.7 | 56.4 | 56.4 | 56.4 | 56.4 |
| 62.8 | 9 | | | | | | | | | | | | | | |
| 49 62. | 49 6 | 49 | 49 | 47 | 47 | 46 | 46 | 46 | 46 | 46 | 42 | 44 | 44 | 44 | 44 |

ALIGNMENTS

| | | precure |
|------|-----|--------------|
| | | 4 |
| | | (EC 3.2.1.1) |
| LT 1 | 305 | a-amylase |

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori C;Species: Aspergillus awamori C;Date: Peb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004 C;Accession: A48305 R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.; J Curr. Genet. 17, 203-212, 1990 A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asperg A;Reference number: A48305; MUID:90254827; PMID:2340591

A;Accession: A48305
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-498 <KOR>
A;Cross-references: UNIPROT:Q02905
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation C;Superfamily: Aspergillue alpha-amylase; alpha-amylase core homology C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation F;194-321/Domain: alpha-amylase core homology <AMY>

Gape ö Length 498; Indels 100.0%; Score 78; DB 2; I 100.0%; Pred. No. 4.1e-05; :ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 13; Conservative

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99 AYHGYWQQDIYSL 111 1 AYHGYWQQDIYSL 13 셤 à

RESULT 2

Alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
NyAlternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
G.Species: Aspergillus oryzae
C.Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C.Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C.Accession: S04548; A3214; JS0240; A91930; A93767; A10627
R.Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A)Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon on A; Reference number: S04548; MUID:89237897; PMID:2785629
A)Accession: S04548
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1499 <WIR>
A; Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295221

A; Genetics: AMY1

A;Accession: A33214 A;Molecule type: mRNA A;Residues: 1-99 <MI2> A;Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921 R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

cyclomaltodextrin

R;Isemura, S.; Ikenaka, T. J. Biochem. 74, 1-10, 1973 A;Reference number: A91930; MUID:74001521; PMID:4733850 A;Accession: A91930

Proc. Jpn. Acad. 51, 285-290, 1975

A,Molecule type: protein A,Residues: 206-225 <ISE> R,Narita, K.

A; Reference number: A93767

A; Accession: A93767

this as isozyme II

A; Molecule type: DNA
A; Residues: 1-499 «GEN»
A; Genetics: AMY2
A; Note: the authors refer to

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A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Description: glycogen/starch degradation c; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology c; Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; metal) F;1-21/Domain: signal sequence #status predicted <SIG> F;2-499/Product: alpha-amylase or #status experimental <MAT> F;194-321/Domain: alpha-amylase core homology <AMY> F;195-59,171-185,261-304,461-496/Disulfide bonds: #status experimental F;142,183,186,231,181 diding site: carbohydrate (Asn) (covalent) #status experimental F;218,183,184,184 site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                A;Cross-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Reference number: JS0240; MUID:8937877; PMID:2789162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: JSO663
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-499 «SHI»
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: alpha-amylase; alpha-amylase core homology
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <&IG>
F;194-3121/Domain: alpha-amylase core homology <AMY>
F;194-3121/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A. Contents: annotation; X-ray Crystallography, 3.0 angstrome C. Comment: One atom of calcium per molecule is essential for activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: amy3; AmyI
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 78; DB 2; Lv
100.0%; Pred. No. 4.1e-05;
iive 0; Mismatches 0;
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A;Residues: 1-499 <GEN>
A;Note: the authors refer to this as isozyme I
R;Matsura, Y; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
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A; Status: translation not shown
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                                                   A, Molecule type: mRNA
A, Residues: 1-499 <WI2>
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A;Residues: 1-499 <WIR>
A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;MOJECULE type: protein
A;Residues: 434-443,446-447,'Q',449-458,'GTTV',459-464,467-468,'B',470,'B',472-499 cNAR>
R;Matsuura, Y:; Kusunoki, M.; Harada, W.; Kakudo, M.
B;Matsuura, Y:; Kusunoki, M.; Harada, W.; Kakudo, M.
B;Motem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annocation; X-ray crystallography, 3.0 angstroms
A;Contents: annocation; X-ray crystallography, 3.0 angstroms
B;Swiff, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkenburg, J.P.; Wilkinson, A.
B;Nobmitted to the Brookhaven Protein Data Bank, August 1992
A;Reference number: A51548; PDB:6TAA
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
A;Reference number: JS0240; MUID:89378767; PMID:2789162
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N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04549; A33215; A44713
R;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Mcrobiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon A;Reference number: S04548; MUID:89237897; PMID:2785629
A;Accession: S04549
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100.0%; Score 78; DB 1; Length 499; 100.0%; Pred. No. 4.1e-05; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 13; Conserv

1 AYHGYWQQDIYSL 13 13; Conservative

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1 AYHGYWQQDIYSL 13

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alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Accession: B48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.; 7
Curr. Genet. 17, 203-212, 1990
A;Reference number: A48305; MUID:90254827; PMID:2340591
A;Reference number: B48305
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
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A;Cross-references: UNIPROT:014154; EMBL:298762; PIDN:CAB11471.1; GSPDB:GN00066; SPDB:SP?
A;Experimental source: strain 972h-; cosmid c4A8
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C, Superfamily: Aspergilius alpha-amylase; alpha-amylase core homology
CKeywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Cryptococcus sp.
A;Variety: strain CS2
C;Date: 23-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
   Gaps
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R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood,
submitted to the EMBL Data Library, August 1997
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C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
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100.0%; Score 78; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0;
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Pred. No. 0.0027;
2; Mismatches 1
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
Mismatches
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A) Cross-references: UNIPROT:Q02906
C) Function:
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Local Similarity 76.9%;
les 10; Conservative
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   Conservative
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   13;
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Best Local S
Matches 10
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   Matches
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                                                                                                                                            NyAlternate names: 91ycogenase; Taka-amylase A
NyAlternate names: glycogenase; Taka-amylase A
C;Species Aspergillus oryzae
C;Species Sapergillus oryzae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JT0466
A;Tada, S; I inutra; Y; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A;Title: Cloning and mucleotide sequence of the genomic Taka-amylase A gene of Aspergill
A;Reference number: JT0466
A;Molecule type: DNA
A;Residues: 1-499 <TADA
A;Residues: 1-499 <TADA
A;Cross-references: UNIPROT:P10529
C;Comment: See also PIR:JK0201 and PIR:JS0240.
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Gene 84, 319-327, 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for A;Reference number: JN0588; MUID:90128276; PMID:2612911
A;Accession: JN0588.
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Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
:1-21/Domain: signal sequence #status predicted <SIG>
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;194-321/Domain: alpha-amylase core homology <AMY>
;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
;231,251,318/Active site: His, Glu, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 100.0%; Score 78; DB 2; Length 499; 1 Similarity 100.0%; Pred. No. 4.1e-05; 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
;Residues: 1-499 <TSUS
;Ccross-references: UNIPROT:0967H4
;Comment: The alpha amylases are encoded by multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYHGYWQQDIYSL 111
   99 AYHGYWQQDIYSL 111
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Best Local Similarity
Matches 13; Conserv
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Gaps

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A;Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g39656
C;Genetics:
A;Gene: SWA2
C;Gene: SWA2
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/fstarch degradation
C;Superfamily: Asperglilus alpha-amylase; alpha-amylase core homology
C;Reywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-20/Domain: slynal sequence #status predicted <SIG>F;1-50/Product: alpha-amylase #status predicted <AMT>
F;205-332/Domain: alpha-amylase eore homology <AMY>
F;205-332/Domain: alpha-amylase (Asn) (covalent) #status predicted
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R;Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A;Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lipon A;Reference number: JC4510; MUID:96105202; PMID:8529895
A;Reference number: JC4510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: JK0201
A; Accession: JK0201
A; Accession: JK0201
A; Accession: JK0201
A; Accession: JK0201
A; Residues: 1-478 - TOD>
A; Residues: 1-478 - TOD>
A; Residues: 1-478 - TOD>
A; Cross-references: UNIPROT: P10529
C; Comment: One atom of calcium per molecule is essential for the activity.
C; Comment: See also PIR: JT0466 and PIR: JS0240.
C; Comment: See also PIR: JT0466 and PIR: JS0240.
C; Comment: See also PIR: JT0466 and PIR: JS0240.
C; Comment: See also PIR: JT0466 and PIR: JS0240.
C; Comment: A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase: alpha-amylase core homology
C; Reymords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F; J73-310/Domain: alpha-amylase core homology <AMY:
F; J17/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 210,230,237/Active site: His, Glu, Asp #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N;Alternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar.1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JK0201
R;Toda, H; Kondo, K; Narita, K.
R;Toda, H; Dpp. Acad. 58B, 208-212, 1982
A;Title: The complete_amino acid sequence of Taka-amylase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pullulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
NiAlternate names: LKA1 protein; raw starch-degrading amylase
NiContains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C.Species: Lipomyces kononenkoae
C.Species: Lipomyces kononenkoae
C.Species: Urbeb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.1%; Score 64; DB 2; Length 507; 69.2%; Pred. No. 0.0084; ive 3; Mismatches 1; Indels
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84.6%; Pred. No. 0.017;
iive 0; Mismatches 2; Indels
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110 AYHGYWMKDIYAI 122
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A;Residues: 1-507
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N.Alternate names: alpha-1,4 glucanohydrolase
C;Species: Schwanniomyces occidentalis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S33921
R;Clarcos, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A;Pitle: Molecular structure of the SWA2 gene encoding an AWY1-related alpha-amylase frc
A;Reference number: S33921; MUD:93365041; PMID:8358835
A;Accession: S33921
A;Molecule type: DNA
                      R; Iefuji, H.; Chino, M.; Kato, M.; Iimura, Y.
Biochem. J. 318, 989-996, 1996
A; Title: Raw-starch-digesting and thermostable alpha-amylase from the yeast Cryptococcus A; Aritle: Raw-starch-digesting and thermostable alpha-amylase from the yeast Cryptococcus A; Reference number: S72270; MUID:96433120; PMID:8836148
A; Residues: DNA
A; Residues: 1-631 < IEF>
A; Residues: 1-631 < IEF>
A; Cross-references: UNIPROT:092394; EMBL:D83540; NID:g1595852; PIDN:BAA12010.1; PID:g159 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJOINT ABPORTAILUS NIGER
C; Species: Aspergillus niger
C; Accession: A35282
R; Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pete Biochemistry 29, 6244-6249, 1990
A; Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom r
A; Reference number: A35282; MUID:91002514; PMID:2207069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: A35282
A,Status: preliminary, nucleic acid sequence not shown; not compared with conceptual tra
A,Molecule type: mRNA
A,Residues: 1-484 <BOE>
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A; Superfamaily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamaily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>
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C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-631/Product: alpha-amylase #status predicted <MAT>
F;206-335/Domain: alpha-amylase core homology <AMY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 2; Length 631;
Pred. No. 0.005;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: amy-CS2
A;Introns: 289/2; 326/2
C;Function:
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Accession: S72270
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A;Residues: 1-624 <STE>

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Search completed: February
Job time: 1.50579 secs
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                                                                                                                                                                                                                                                                                                                               A; Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages A; Pasthway: glycogen/starch degradation
G; Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C; Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C; Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F; 128/Domain: signal sequence #status predicted <a href="Millor">MILLOR</a>
F; 48-141/Domain: alpha-amylase starch-binding domain homology <a href="Millor">MILLOR</a>
F; 320-447/Domain: alpha-amylase core homology <a href="Millor">MILLOR</a>
F; 310-447/Domain: alpha-amylase core homology <a href="Millor">MILLOR</a>
F; 310-447/Domain: alpha-amylase (ore homology <a href="Millor">MILLOR</a>
F; 310-444/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 357, 377, 444/Active site: His, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C;Species: Thermoactinomyces vulgaris
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S3478
R;Hofemeister: B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A;Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A;Reference number: S31478
A;Recession: S31478
A;Recession: BNA
A;Residues: 1-482 <HOF>
A;Description: C;Punction:
C;Punction:
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C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Jaccession: S0064
R;Itch, T: Yamashita, I:; Fukui, S.
FEBS Lett. 219, 339-342, 1987
A;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycop
A;Reference number: S00064; MUID: 87276512; PMID: 3497057
Cross-references: UNIPROT: 001117; GB: U30376; NID: 91173536; PIDN: AAC49622.1; PID: 911735
Experimental source: strain IGC4052B
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A, Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C, Keywords: glycosidase; hydrolase; polysacharide degradation
F;194-319/Domain: alpha-amylase core homology <AMY>
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Pred. No. 0.053;
1; Mismatches 3; Indels
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Best Local Similarity 69.2%; Pred. No. 0.022;
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                                                                                                                A;Molecule type: protein
A;Residues: 29-44 <ST2>
A;Experimental source: IGC4052B
C;Genetics:
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Best Local Similarity 69.27
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A; Molecule type: DNA
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A; Residues: 1-494 < ITC)
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A; Residues: 1-494 < ITC)
A; Crose-references: UNIPROT: P21567; EMBL:X05791; NID:94847; PIDN:CAA29233.1; PID:94848
A; Crose-references: UNIPROT: P21567; EMBL:X05791; NID:94847; In having 368-Thr
C; Genetics:
A; Gene: ALP1
C; Genetics:
A; Gene: ALP1
C; Function:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C; Rowords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metallc
C; Rowords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metallc
F; 27494/Product: alpha-amylase core homology < AMT-F; 27-494/Product: alpha-amylase core homology < AMT-F; 27-
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Q87fr2 Q7mcl0 Q8d511 Q9k186 P09k186 P068323 P31835 P31835

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                      HISSP, PIOSOS, TATA.

InterPro; IPR006589; Alp_amyl_cat_gub.

InterPro; IPR006679; Alpha_amyl_cat.

InterPro; IPR0066047; Alpha_amyl_aat.

InterPro; IPR00128; Alpha-amylase; I.

PRINTS; PR00110; Alpha-amylase; I.

SMART; SM00642; Aamy; I.

Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase; Hyddrolase; Multigene_family; Signal;
                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
1011. TaxID=105351,
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Q02906 aspergillus
Q96ch4 aspergillus
Q76199 aspergillus
Q71v45 aspergillus
Q90v07 emericella
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                                                2005, 18:25:28; Search time 7.62934 Seconds (without alignments) 872.556 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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AMYA_ASPNG
AMY2_DEBOC
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AMY1_LIPKO
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AMY1_SCHPO
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AMY4_SCHPO
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Maximum Match 100%
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                                   protein search, using sw model
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Q71V45
Q9UV07
Q15751
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Potential.
Alpha-amylase A.
Nucleophile (By similarity).
By similarity.
Calcium 1 (By similarity).

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MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4; TBUKAGOSHI N., Furnkawa M., Nagaba H., Kirita N., Tsuboi A., Udaka S.; "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple related genes."; Gene 84:319-327(1989).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Takahashi K., Hara S., Yoshizawa K.; Tada S., Limura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.; Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae.";
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MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
BIZOZOWSKI A.M., Davies G.J.;
BIZUCCOWSKI A.M., Davies G.J.;
"Structure of the Aspergillus oryzae alpha-amylase complexed with the inhibitor acarbose at 2.0-A resolution.";
Biochemistry 36:10837-10845(1997).
-!- CATALYTIC ACTIVITY: Endochydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
Genes M.J., Dove M.J., Seligy V.L.;
"Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing eight introns.";
Gene 79:107-117(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 206-225.
MEDLINE=74001521; PubMed=4733850;
ISemura S., Ikenaka T.;
"The amino acid sequess of glycopeptides obtained from Taka-amylase
A with trypsin and chymotrypsin.";
J. Biochem. 74:1-10(1973).
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                             Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                         STRAIN=DSM 63303;
MEDLINE=89237897; PubMed=2785629;
Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.;
Wirnee alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon organization.";
Mol. Microbiol. 3:3-14(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
MEDLINE=84212370; PubMed=6609921;
Mateuura Y., Kueunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Biochem. 95:697-702(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Narita K.;
Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975)
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P.10529; P11763; Q00250;
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1989 (Rel. 45, Last senotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus kawachi (Aspergillus awamori var. kawachi).
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                 (B)
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                           Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (B similarity).
Calcium 2 (By similarity).
By similarity.
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Calcium 1 (via carbonyl oxygen)
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SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       this this concentrations.

Subuntr. Monomer.

Subuntr. Monomer.

BIOTECHNOLOGY: Used in the brewing industry to increase the fermentability of beer worts (including those made from unmalted cereals), in the starch industry to make high maltose and high DE syrups (starch saccharification), in the alcohol industry to reduce fermentation time, in the cereal food industry for low temperature modification and improvement of chilled and frozen dough, and in the forestry industry for low-temperature modification of starch. Sold under the name Fungamyl by Novozymes.

MISCELLANDROUS: The sequence of AMY1 and AMY2 is shown.

SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
                                                                                                                                                                                                                                                                 BIR; JYCO210; JYCO201.

BIR; JYCO210; JYCO201.

BIR; JYCO466; JYCO461.

BIR; JYCO466; JYCO48.

BIR; JYCO488; ALAS1.

R PB; ZAA, X-ray; &=22-499.

R PB; JTAA, X-ray; &=22-499.

R PB; JTAA, X-ray; &=22-499.

R PB; JTAA, X-ray; &=22-499.

R PB; JYCO311cD; PRO06064; Alpha amyl_cat_sub.

R InterPro; IPRO06049; Alpha amyl_cat_sub.

R InterPro; IPRO06049; Alpha-amylase; IRRO110; Alpha-amylase.

R SWART; SWO0612; And SWARTLASE.

R SWART; SWO0642; And; 1.

B Jostructure; Calcium-binding; Carbohydrate metabolism;

Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;

M Multigene family; Signal.

T CHAIN.

Z 499 Alpha-amylase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium 1.
Calcium 1 (via carbonyl oxygen).
Calcium 1.
Calcium 2.
Calcium 1 (via carbonyl oxygen).
Calcium 1 (via carbonyl oxygen).
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Y (in Ref. 3).
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Y -> PYI (in Ref. 5).
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Q -> R (in AMY3).
F -> L (in AMY3).
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.,
"Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus aniger var. awamori.";
Curr. Genet. 17:2012(1990).
-! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-! COFACYOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-! SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
1 21 Potential.
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Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5070;
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Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By
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Calcium 1 (via carbonyl oxygen)
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25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
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InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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01-APR-1993 (Rel. 25, Last seq.
25-OCT-2004 (Rel. 45, Last anno
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Matches 13; Conservative
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Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
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By land arity.
By similarity.
                              Shibuya I., Tamura G., Ishikawa T., Hara S.;
"Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its
expression in Saccharomyces convisies ";
Biosci. Biochechnol. Biochem. 56:174-179[1992].
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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HSSP; P10529; 7TAA.
InterPro; IPR006689; Alp amyl_cat_gub.
InterPro; IPR0066046; Alpha amyl_cat.
InterPro; IPR0066046; Glyco hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
Hydrolase; Signal.
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Bukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
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Nucleophile (By similarity).

Proton donor (By similarity).

By similarity.

Calcium 1 (By similarity).

Calcium 1 (via carbonyl oxygen)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Taka-amylase A (EC 3.2.1.1).
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MEDLINE=92323146; PubMed=1368777;
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                                                                                                                 "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
                         MEDLINE=20289310; PubMed=10830498;
Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
Iimura Y.;
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Biotechnol. Biochem. 64:816-827(2000).
--- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
--- BIBL: ABO1976; BaA95703.1;
--- PIR; JN0588; JN0588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 78; DB 2; Length 499; 100.0%; Pred. No. 0.00017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                   HSSP, P10529, 7TAA.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0016798; F:alpha-amylase activity, acting on gl

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR006047; Alpha_amyl_cat.

InterPro; IPR006047; Alpha_amyl_cat.

InterPro; IPR006046; Glyco_hydro_l3.

Pfam; PF00128; Alpha-amylase; I.

PRINTS; PR00110; ALPHAAMYLASE.
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499 AA; 54794 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-amylase precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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SEQUENCE FROM N.A.
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Q76L99;
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Q76L99
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CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

DR EMBL; ARI3925; ARI4164-1; --

DR GO; GO:0004556; F:alpha-amylase activity, IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006689; Alpha-amylace activity.

DR InterPro; IPR006689; Alpha-amylace activity.

DR InterPro; IPR006689; Alpha-amylace il.

DR InterPro; IPR006103; Alpha-amylace; I.

R SMART; SM00642; Aamy; I.

W Glycosidase; Hydrolase.

O SEOURNEY.
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Fakhoury A.M., Woloshuk C.P.;
"Amyl, the alpha-amylase gene of Aspergillus flavus: Involvement in aflatoxin biosynthesis in maize kernels.";
Phytopathology 89:908-914(1999).
                                                                                                                                                                               Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5059;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boase N.A., Murphy R.M., Kelly J.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AF208225; AAF17103.1; --.
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                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase (EC 3.2.1.1).
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Last annotation update)
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499 AA
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PRT;
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PRELIMINARY;
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                                                                                                                                                          Aspergillus flavus.
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Matches 13; Conserv
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1 AYHGYWQQDIYSL 13

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014154; 084R6;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annobtation update)
Probable alpha-amylase med30 precursor (EC 3.2.1.1) (1,4-alpha-D-
glucan glucanohydrolase) (Meiotic expression up-regulated protein 30).
Name=ande5; Synonyms=med130, ORFNames=SpRAC25H1.09, SPAC4AB.01;
Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Pungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                              Gaps
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STRAIN=972;
MEDLINE=2124;
MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Brooks K., Enrown D., Brown R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
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                                                                                 Score 75; DB 2; Length 490;
Pred. No. 0.00053;
                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location W.F., Iranfar N.;
Location W.F., Iranfar N.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, PR020289, ABR70852.1;
DictyBase; DDB0214924; amyA.
GO; GO:0004556; Fralpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amylase;
PFfam; PF00128; Alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
SEQUENCE 490 AA; 54249 MW; AB91C4ACEAEB5305 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                              y Match
Local Similarity 92.3%;
hes 12; Conservative
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                                                                                                                                                                                                                                                              91 AYHGYWQQDIYAL 103
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Best Local Similarity 83.3
warches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AX4;
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                                                                                       Query Match
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Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Monory P., Moule S., Muraphy L., Niblett D., Oddil C., A. Oliver K., O'Neil S., Managall K., Murphy L., Niblett D., Oddil C., A. Oliver K., O'Neil S., Managall M.A., Rabbinowitsch B., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Welfens I., Beck A., Lehrach H., Reinhardt R., Pohl T.H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Berrym K., Langer I., Mandler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Ashacveski G.V., Usberry D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 29:2327-2337(2001).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SN00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Meiosis; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe T., Miyashita K., Saito T.T., Yoneki T., Kakihara Y., Nabbeshima K., Kishi Y.A., Shimoda C., Nojima H.; "Comprehensive isolation of melosis-specific genes identifies novel proceins and unusual non-coding transcripts in Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
By similarity.
By similarity.
By similarity.
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Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21270454; PubMed=11376151; DOI=10.1093/nar/29.11.2327;
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Nucleophile (By similarity).
Proton donor (By similarity).
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InterPro; IRR0066047, Alpha amyl_cat.
InterPro; IPR006589; Alp amyl_cat_sub.
Pfam; PF00128; Alpha-amylase; 1.
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EMBL; Z98944; CAD62442.1; -.
EMBL; AB054314; BAB60880.1; -.
PIR; T38770, T38770.
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Glycosidase; Hydrolase-
ACT_SITE 206 230
ACT_SITE 297 230
ACT_SITE 297 297
METAL 121 121
METAL 175 162
METAL 206 206
METAL 210 210
METAL 210
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P567JU-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
Aspergillus niger.
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes, Tremellomycetidae, Tremellomycetidae incertae sedis, Cryptococcus, NCBI TaxID=87049;
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STRAIN=S-2;
MEDLINE=96431120; PubMed=8836148;
MEDLINE=9643114., Chino M., Kato M., Iimura Y.;
"Raw-starch-digesting and thermostable alpha-amylase from the yeast Cryptococcus sp. S-2: purification, characterization, cloning, and
  454 488 By similarity.
162 162 N-linked (GlcNAc. ..) (Potential).
357 N-linked (GlcNAc. ..) (Potential).
513 AA, 58715 MW, 455DD97FA428C182 CRC64;
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                                                                                                        85.9%; Score 67; DB 1; Length 513; 76.9%; Pred. No. 0.012; Live 2; Mismatches 1; Indels
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8196B7B6E1D707E5 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD001568; Glyco_hydro_CBD; 1.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                                                                                                                                                   Created)
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67658 MW;
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Blochem. J. 318:989-996(1996).
EMBL, D83541; BAA12011.1; -.
EMBL; D83540; BAA12010.1; -.
PIR; S72270; S72270.
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01-FEB-1997 (TrEMBLrel. 02,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                            Local Similarity 76.9
                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-amylase precursor.
Name=amy-CS2;
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les 10; Conservative
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631 AA;
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Q92394;
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DT 25-OCT-
DE ACID ASPOND
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                  MEDLINE=93365041; PubMed=8389835; Claros M.G., Abarca D., Fernandez-Lobato M., Jimenez A.; Claros M.G., Abarca D., Fernandez-Lobato M., Jimenez A.; Claros M.G., Abarca D., Fernandez-Lobato M., Jimenez A.; Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase from Schwanniomyces occidentalis."; Curr. Genet. 24:75-83(1993).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Burotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=105351;
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Calcium 1 (By similarity).

Calcium 2 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Sancium 2 (By similarity).

Sancium 2 (By similarity).

By similarity.

Norobable).
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Alpha-amplase 2.
Alpha-amplase 2.
Nucleophile (By similarity).
Proton donor (By similarity).
By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (E
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase precursor.
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PIR; S33921; S33921.
HSSP; P10529; TTAA.
InterPro; IPR006699; Alp amyl cat sub.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR066046; Glyco Aydro_13.
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  STRAIN=ATCC 26077 / CBS 2863;
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110 AYHGYWMKDIYAI 122
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les 9; Conservative
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 2 precursor (BC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64; DB 1; Length 484; Pred. No. 0.035; 2; Indels
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| 1] | SEQUENCE FROM N.A. | SEQUENCE T.; | Matsubara T.; | Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. | SMBL; AB083166; BAD066005.1; -. | SMBL; AB083166; BAD066005.1; -. | SMBL; AB083166; BAD06003.1; -. | SERPEROFORM OF SECTION OF S
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Search completed: February 8, 2005, 18:41:53 Job time : 8.62934 Becs

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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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| Description | AX140291 Seguence | D10461 A. shirousa | AB083159 Aspergill | X12725 Aspergillus | AB109452 Aspergill | D00434 Aspergillus | E02659 DNA sequenc | X12726 Aspergillus | X12727 Aspergillus | AB021876 Aspergill | M33218 A.oryzae Ta | AF139925 Aspergill | X52756 A.niger amy | X52755 A.niger amy | AX711606 Sequence | AB083160 Aspergill | E09025 cDNA encodi | AY155463 Lipomyces | U30376 Lipomyces k |
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| σι | AX140291 | ASNAMY | AB083159 | AOAMY1 | AB109452 | ASNTAA | E02659 | AOAMY2 | AOAMY3 | AB021876 | ASNTAAG1 | AF139925 | ANAMYB | ANAMYA | AX711606 | AB083160 | E09025 | AY155463 | LKU30376 |
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| å Query Match | 100.0 | 97.4 | 94.2 | 62.5 | 62.2 | 61.4 | 61.3 | 57.3 | 57.2 | 57.2 | 57.0 | 56.9 | 56.5 | 52.4 | 43.8 | 38.6 | 38.1 | 26.6 | 25.1 |
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| 377.4 21.8 4215 6 E01742 E01744 DNA encoding 377.4 21.8 4223 8 SFALP1 E0159 E01774 DNA encoding 377.4 21.8 4223 8 SFALP1 E0185 DNA encoding 27.4 21.6 1404 6 E01857 E018057 DNA encoding 375.4 21.6 1404 6 E018057 E018057 DNA encoding 275.4 21.6 1404 6 E018057 E018059 DNA encoding 275.4 21.6 1404 6 E018059 E018059 DNA encoding 277.8 21.6 1404 6 E018059 E018059 DNA encoding 273.8 21.6 1404 6 E018059 E018059 E018059 DNA encoding 273.8 21.6 1404 6 E018059 DNA encoding 273.8 21.6 1404 6 E018059 E | AX140291 Sequence 1 from Patent W00134784. AX140291 AX140291.1 GI:14280549 Aspergillus oryzae Aspergillus oryzae Aspergillus oryzae Bukaryota; Wingl; Ascomycota; Pezizomycotina; Burotiomycetes; Burotiales: Trichocomaceae: Aspergillus. | e e e e e e e e e e e e e e e e e e e | / Match 100.0%; Score 1734; DB 6; Length 1734; Local Similarity 100.0%; Pred. No. 0; Les 1734; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
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Kashiwa, Chiba 277
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                         GTCAACCTCCGGCAGCAGCACGACCTCTACAACATGATCAACACCGTCAAATCCGACTG
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                                                                                         AGGCGTGTACTGTATCGGCGAGGTGCTCGACGGTGATCCGGCCTACACTTGTCCTACCA
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                                                                                                                                              TGGGTCGACGACTGCGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGAACATGGCA
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                                                                             TGCGGACTGGCGATCGCAATCCATTTATTTCCTTCTCACGGATCGATTTGCAAGGACGGA
                                                                                                                               TGGGTCGACGACTGCGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGAACATGGCA
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VARFTILNOGOTPITYAGOEGHYAGGNDPANREATWLGSCPTNDSELYKLJASANAIRNY
AISKOTGFVTYKNMI YKKDDTIABKGTDGSGJUVTLISNKGASGDSYTLSLSGAGYT
AGGQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS"
                                                                                         1680
                                                                                                                                                                                                            bp mRNA linear PLN 26-DEC-2003 gene for alpha-amylase, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (04-APR-2002) Takayoshi Matsubara, Osaka City University,
staculty of Science; 3-3-138 Sugimoto, Sumiyoshi-ku, Osaka, Osaka
558-8585, Japan (E-mail:nobufrog@mail.goo.ne.jp,
Tel:81-6-6605-2585)
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                GTACTGCTATTCAATCTGGCATTGGACAGTGAGTTTGAGTTTTGATGTACAGTTGGAGTCG
                                                               CACATCAAGCTCTCCCTTCTCTGAACAATAAACCCCACAGAAGGCATTTATGATGGTCGC
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Unpublished
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/mol_type="mRNA"
/strain="KT-11"
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                                                                                                                 Score 1633.2;
Pred. No. 0;
0; Mismatches
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/codon_start=1
/product="alpha-amylase"
/protet=ingia="BAD06002.1"
/db_xref="G1:40313276"
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1. 1638
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/gene="amyl I"
/gene="amyl I"
50. 1549
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ABGPEGILLUB awamori amyl I gene
AB083159
AB083159.1 GI:40313275
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/gene="amyl I"
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Best Local Similarity 99.8%;
Matches 1635; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 1638)
Matsubara, T.
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/gene="amy1"
join(678 .782,838 .876,962 .1077,1147 .1255,1324 .1552,
1611 .1773,1839 .1985,2051 .2291,2371 .2655)
/gene="amy1"
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/gene="amy1"
/number=7
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/gene="amy1"
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Aspergillus oryzae amyl gene for alpha-amylase (EC 3.2.1.1).
X12725
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Aspergillus oryzae
Aspergillus oryzae
Aspergillus oryzae
Bukaryotta; Fungi, Ascomycota, Pezizomycotina; Eurotiomycetes;
Eukaryotta; Fungi, Ascomyceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases I to 3366)
Wirsel, S., Lachmud, A., Wildhardt, G. and Ruttkowski, E.
Three alpha-amylase genes of Aspergillus oryzae exhibit identical
intron-exon organization
99237897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1501 GTATCCGACTGAGAAGTTGGCAGGTAGCAAGATCTGTAGTAGCTCGTGAAGGGGGGGAG 1560
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              CCGCGAAGCAACCTGGCTTCCGGGCTACCCGACAGCGAGGCGTGTACAAGTTAATTGC 1201
                                                                                                                                                                                                                                                                                                                                                                              GAACTGGCCCATCTACAAAGACGACAACGATCGCCATGCGCAAGGGCACAGATGGGTC 1321
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                                                                                                                                                                                              CTCCCCCAACGCAATCCCGCAACTATCCCATTAGCAAGATACAGGATTCGTGACCTACAA
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Location/Qualifiers
1. .3366
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Direct Submission
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ACCESSION
VERSION
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ORGANISM
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AUTHORS
TITLE
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| exon | Jene= amy | Qy 341 AGNTGCCTACCATGGCTACTGGCAGGARAT |
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| 1437 ACCGTGACGTTGGTTCGATGGAAATGTGCCTGTTCCTATGGCAGGTGGGCTACCTAGG 196 | AB109452 AB109452 AB109452 AB109452 AB109452 AB109452 ACCESSION ADDRALLING RAWACHII amyA gene for alpha-amylase, complete cds. ACCESSION AB109452.1 G1:30175084 AERONECESTON AB109452.1 G1:30175084 AUTHORS ADDRALISH RAWACHII ADDRALISH RAWACHII AUTHORS ALO KARACHII RAWACHII AUTHORS AUTHOR | GQQLTEVICCTIVIVGSDGNVPVPWAGGLPRVLYPTEKLAGSKICSSS" <556720 /gene="amyA" intron 721775 /gene="amyA" |

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1562. .1802
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                                                                                                                                                                                                                                                                                                                          Query Match 61.4%; Score 1065.4; DB 8; Length 2337; Best Local Similarity 75.3%; Pred. No. 8.1e-247; Matches 1701; Conservative 0; Mismatches 6; Indels 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ATGGGTCGACGACTGCGACTTGTAATACTGCGGATC----
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YPLLNAFKSTGGSMDDLYNMINTVKSDCPDSTLLGTFYENHDNPRFASYTNDTALAKN
VAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIASANAIRNY
                                                                                                                                                                                                    AISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTIISNKGASGDSYTISLSGAGYT
AGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS"
                                                                                                                                                                                                                                      121. .180
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1122. .1284,1350. .1496,1562. .1802,1882. .2166)
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1108. .1113

'note="consensus sequence PuCTPuAC of fungal IVS"
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    441.
    447
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E02659.1 GI:2170887
B02659.1 GI:2170887
Appergillus oryzae
Aspergillus oryzae
Aspergillus oryzae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
Takahashi,K., Iimura,M., Gomi,K., Hara,M., Yoshizawa,K., Tada,S.
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NOVEL GENE AND VECTOR, TRANSFORMING SUBSTANCE USING SAME GENE AND VECTOR AND USE THEREOF.

Patent: JP 1990268685-A 1 02-NOV-1990;

TAX ADM AGENCY, JOZO SHIGEN KENKYUSHO: KK

S Appergillus oryzae

PN JP 199026865-A/1

PD 02-NOV-1990
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/product='takaamylase A'.
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/mol_type="genomic DNA"
/db_xref="taxon:5062"
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| CAACTTGGCTGATCGATGATACTTACGAAATCAGTTGACGGCCTCCGTATCGACAGTA AAACACGTCCAGAAGGACTTCTGGCCCGGGTACAAAGCCGCAGGCGTGTACTGTATC | 798 GGCGAGGTGCTCGACGGTGATCGGCCTACACTTGTCCCTGAACGTCATGGACGGC BS.7 1208 GGCGAGGTTCGACGTTGATCCGGCCTACACTTGTCCCTACCAGAACGTCATGGACGGC 1267 1208 GGCGAGGTGCTCGACGTTGATCCGGCCTACACTTGTCCCTACCAGAACGTCATGGACGGC 1267 858 GTACTGAACTATCCCAT | 1268 GTACTGAACTATCCATCTTCCTCCAACCATGAGCCTTCTTGCAAGTCTCATCT 1327 875TTACTATCCACTCCAACGCCTTCAAGTCAACCTCCG 912 1328 CTAACGAAACGACTAAAAACCAGTTACCAATCCAACGCCTTCAAGTCAAGTCAACTCCG 1387 | GCAGCATGGACGACCTCTACAACATGATCAACGTCAAATCCGACTGTCCAGACTCAA GCAGCATGGACGACTCAA GCAGCTCAAATCCGACTGTCCAGACTCAA GCAGCATGGACGACTCTACAACATGTCAAATCCGAATTGTCCAGACTCAA | 973 CACTCCTGGGCACATTCGTCGAGAACCACGACAACCCCGGGTTCGCTTC 1021 | CITITATITICCGTTCCCAATITCCACACAGAACCCCACCTAACAAGAGCAAAGTTACAC | CAACGACATAGCCTCGCCAAGAACGTCGCAGCATTCATCATCATCTCAACGAATCCC | CATCATCTACGCCGGCCAAGAACAGCACTACGCCGGGAAACGAAACGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGGGAAACGAAACGGAAACGGAAACGGAAACGGAAACGGAAACGGAAACGGAAACGGAAACGGAAACAAC | AGCAACCTGGCTCTCCGGCTACCGGACGGAGCTGTACAAGTTAATTGCCTCCGC | GAACGCAATCCGGAACTATGCCATTAGCAAGATACAGGATTCGTGACCTACA GAACGCAATCCGGAACTATGCCATTAGCAAGATACAGGATTCGTGACCTACA-GGAACTAAG | CACAACCTCTAAGCATACCCTAATGGCCTATCTTCAGAGTATCTGACACAAGAGACTAAT | AGAATGGCCCATCTACAAGACGACAAGGATGGCCATGGGCAAGG | GCACAGATGGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGGTTCGT | ATACCCTCTCCTTGAGTGGGGGTTACACAGCGGGCCGGCAGTTGAGGGGGGTTGAGGGGGTTGAGGGGGGTTGAGGGGGG | GCTGCACGACGACGGTTGGTTCGGATGGAAATGTGCCTGTTCCTATGGCAGGTGGGC | TACCTAGGGTATTGTATCCGACTGAGAAGTTGGCAGGTTAGCAGATCTGTAGTAGCTCGT [| 1549 GAAGGTGGACAGTNTATGATGGTA-TTCATTTGGCATTGGACAGTGAGTTTGA 1608 |
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| Best Local Similarity 75.3%; Pred. No. 2e-246; Matches 1700; Conservative 0; Mismatches 7; Indels 552; Gaps 8; Qy 1 TCACATCAAGCTCTCCTTCAACAATAAACCCCACAGAAGGCATTTATGATGGTG 60 Db 68 TCACATCAAGCTCTCCTTCAACAATAAACCCCACAGAAGGCATTTATGATGATGATGATGATGATGATGATGAAGCTCTCCCTTCTCTGAACAATAAACCCCACAGAAGGCATTTATGATGATGATGATGATGATGAAGAAGTGATGATGA | OY 61 CGTGGTGGTCTCTAITTCTGTACGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCAACGC 120 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 188 CTGCGGACTGGCGATCGCATTTATTTCCTTCTCACGGATCGATTTGCAAGGACGG 181 ATGGGTCGACGACTTGTAATACTGCGGATC | Db 248 ATGGTCGACGACTGCGACTTGTAATACTGCGGATCGGTGTTGTTGCTACTACTAGCTT 307 Qy 217AGAAATACTGTGGTGGAACATGGCAGGC 245 Db 308 TCAGAAAGAGGAATGTAAACTGACTTGATATAGAAATACTGGTGGAACATGGCAGGC 367 | Oy 246 ATCATCGACA 255 | Oy 256 | QY 281 CTTCACAGCCATCTGGATCACCCCCGTTACAGCCCAGCTGCCCCAGACCACGCATATGG 340 Db 488 CTTCACAGCCATCTGGATCACCCCCGTTACAGCCCCAGACCCCCAGACCACACGCTATGG 547 | Qy 341 AGATGCCTACCATGGCAGCAGCAGATAT | Qy 374ATACTCTGG 383 Db 608 TCTACCTGTCATCTATTCTACATCATAGAACTTGATGGTTTTAGATACTCTCTG 667 | OY 384 AACGAAAACTACGGCACTGCAGATGACTTGAAGGGGTCTCTTCGGCCCTTCATGAGAGG 443 Db 668 AACGAAAACTACGGCACTGCAGATGACTTGAAGGCGCTCTTCGGCCCTTCATGAGAGG 727 | Qy 444 GGGATGTATCTTATGGTCGATGTGCTTACTAACCATAT | Qy 482GGGCTATGAGGAG 495 Db 788 ACTTCGCGGATATGGTTCATTTCAGTACTGACAATGAGTAATATCAGGGCTATGATGAGAG 847 | OY 496 CGGGTAGCTCAGTCGATTACAGTGTGTTTAAACCGTTCAGAGACTACCTAC | Qy 556 CGTTCTGTTTCATTCAAAACTATGAAGATCAGACTCAGGTTGAGGATTGCTGGCTAGGAG 615 | Qy 616 ATAACACTGTCTCCTTGCCTGATCTCGATACCACCAAGGATGTGGTCAAGAATGAAT | Oy 676 ACGACTGGGTGGGATCATTGGTATCGAACTACTCCA | Oy 712 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(552. 782,838. .876,962. .1077,1147. .1255,1324. .1552,
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Direct Submission
Submitted (26-MG-1988) Wirsel S., Inst. f. Biochemie, TH
Submitted (26-MG-1988) Wirsel S., Inst. f. Biochemie, TH
Darmstadt, Petersenstr. 22, D-6100 Darmstadt, FRG
see X12725 - x12727 for A. oryzae amyl, amy2 and amy3 genes. No
amy2 transcripts were detected in Northern blot analyses; exons and
introns in FT are given accordingly amyl gene (X12725) Data kindly
reviewed (28-Mar-1989) by Wirsel S.
Location/Qualifiers
                                                                                                                                                                                                                                                Aspergillus oryzae amy2 gene for alpha-amylase (EC 3.2.1.1).
X12726
X12726. GI:2442
                                  1668
                                                                            2287
                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae
Aspergillus oryzae
Aspergillus oryzae
Aspergillus oryzae
Aspergillus oryzae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (Bases I to 3160)
Wirsel, S., Lachmud, A., Wildhardt, G. and Ruttkowski, E.
Three alpha-amylase genes of Aspergillus oryzae exhibit identical
intron-exon organization
### (1989)
### (1989)
                                                             2228 GITIGATGTACAGTIGGAGTGGTTACTGCTGTCATCCCCTTATACTCTTCGATTGTTTT
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KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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TITLE
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Pred. No. 4e-229;
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Best Local Similarity 74.8
Matches 1617; Conservative
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Wirsel,S., Lachmund,A., Wildhardt,G. and Ruttkowski,E.
Three alpha-amylase genes of Aspergillus oryzae exhibit identical
Intron-exon organization
Mol. Microbiol. 3 (1), 3-14 (1989)
89237897
                                                                                                  Wirsel, S.
Direct Submission
Submitted (126-040-1988) Wirsel S., Inst. f. Biochemie, TH
Submitted (126-040-1988) Wirsel S., Inst. f. Biochemie, TH
Darmstadt, Petersenstr. 22, D-6100 Darmstadt, FRG
see x12725 - x12727 for A oryzae amyl, amy2 and amy3 genes. amy3
transcripts were detected in Northern blot analyses [2]. Data
kindly reviewed (28-Mar-1999) by Wirsel S.
Location/Qualifiers
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1. .35244
/organism="Aspergillus oryzae"
/mol_type="genomic DNA"
/strain="RiB40"
/db_xref="taxon:5062"
complement(join(11172. .11549,11634. .12084,12151. .13136))
/gene="amyR"
/gene="amyR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus oryzae
Biosci Biotechnol Biochem. 64 (4), 816-827 (2000)
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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Gomi, K. and Akeno, T.
Direct Submission
Submitted (15-DEC-1998) Katsuya Gomi, Tohoku University, Graduate
School of Agricultural Science; 1-1, Tsutsumidori-Amamiyamachi,
Abba-ku, Sendai, Miyagi 981-8555, Japan
(B-mail:gomi@blochem.tohoku.ac.jp, Tel:81-22-717-8901,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gomi, K., Akeno, T., Minetoki, T., Ozeki, K., Kumagai, C., Okazaki, N.
and Iimura, Y.
                                                                                                2364 ATACAGAACTGGCCCATCTACAAAGACGACACAACGATCGCCCATGCGCAAGGGCACAGAT
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AmyRp; alpha-glucosidase; Taka-amylase A.
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Aspergillus oryzae
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2110 GATATGGTTCATTTCAGTACTGACAATGAGTAATATCAGGGCTATGATGAGGGGGGTAGG
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|gene="agdA"
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/gene="agdA"
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21149. ,21377,21436. ,21598,21664. ,21810,21876. ,22116,
22196. ,22483)
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                                                                                                                                                       PTSPPSTVADAQYLHPDFSESFTRLPPPDLVSSPDSTNSLFDSSTIGALPAPRRLSTP
NLAHVNVELKKILFPIMPVVRQDQLQQDCHQPERLSPQRYARIAALGAATHTQLKLDG
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HLPVLVGKAVMGVIAAASQGAVDAHGIGMEQKLYDLGTSVADVSRSLSTKAAHHLAES
TIDPRELLWGILTTISRIRGSQSYLPPALVEGSRGIISFDCSLISISPLPSFGGGPPAI
MWRTGESGFDLLGIADDLQERENEGGEGIIVVAGEEISF"
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I PMFGVDTCGFNGNTDEELCNRWMQLSAFFPPYRNHNVLSAI PQEPYRWASVI DATKA
ARNI IXYAI LEYFYTLEHLAHTTGSTVWRALAMEFPNDPSLAANGTQFPUGESVWI IV
LEPOTVQCYP FQVGHGEWYDWYSOTGOANGAKPGVNTTI SAPLGHI PVFYRGGSI LP
MQEVALTTROARKTPRASILASILSSNGTASGQLYLDDGESVYPEDTLSNDFLASRSTLE
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SSTARCHTADRKXCGGTWAGGIIDKLDYIQGMGFTAINTYPTAQLPGTAYGDAXHG
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PSSQDYFHPFCLIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSN
YSDGALDITYGHYQKDPWPGYNKAGAGYVCIGSTLDGDPATTCPYQUNMGGYLMYPDIY
YPLLAMFKSTGGSMDDLYNMINTYVKSDCPDSTLLGTFVENHDNPFFASYTNDTALAKN
VAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYFTDSELYKLIASANAIRNY
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AGQQLTEVIGCTTVTVGSDGNVPVPWAGGLPRVLYPTEKLAGSKICSSS"
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/note="transposon-like element"
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22196. .22483)
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21410 CTGATCGATGATACTTACGAAATCAGTTGACGGCCTCCGTATCGACAGTAAAAAAGGGT

-----TIGACGGCCTCCGTATCGACACAGTAAAACACGT

712

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746

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8

Gaps

CCAGAAGGACTTCTGGCCCGGGTACAACAAGCCGCAGGCGTGTACTGTATCGGCGAGGT

802

711

Query Match 57.2%; Score 992.4; DB 8; Length 35244; Best Local Similarity 74.8%; Pred. No. 5.9e-229; Matches 1617; Conservative 0; Mismatches 1; Indels 544;

21470 CCAGAAGGACTTCTGGCCCGGGTACAAAGCCGCAGGCGTGTACTGTATCGGCGAGGT 21529

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.1248,1317. .1545,
.2647)
                                                                                           Aspergillus oryzae
Aspergillus oryzae
Aspergillus oryzae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiales; Trichocomaceae; Aspergillus.
1 (bases 1 to 2335)
Tsukagoshi,N., Furukawa,M., Nagaba,H., Kirita,N., Tsuboi,A. and
                              PLN 27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            773. .827
|note="Taa-G1 intron A (no splice consensus); putative"
                                                                                                                                                                              Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple related genes Gene 84 (2), 319-327 (1989)
                                                                                                                                                                                                                                                          source text: A.oryzae (strain JCM02239) DNA.
Location/Qualifiers
1. .2935
                     /organism="Aspergillus oryzae"
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1603. .1765.1830. .1976.2041. .2281,2360.
/note="Taka-amylase A (Taa-G1) precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <607. 772
/note="Taka-amylase A (Taa-G1) precursor"</pre>
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/note="Taka-amylase A signal peptide"
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join(772,828. .868)
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join(1975. 1976,2041. 12281)
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//note="Taka-amylase A precursor"
/number=2
869. .954
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product="Taka-amylase A"
oin(1545,1603. .1765,1830)
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product="Taka-amylase A"
                                                                  M33218.1 GI:166530
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                                                                                 Taka-amylase A.
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                                                                                21590 CTATCCCATGTATGGTTCCTCCAACCATGAGCCTTCTTGCAAGTCTCATCTCCTAACGAA 21649
                                                                                                                                                                           21710 GACGACCTCTACAACATGATCAACACGGCGTCAAATCCGACTGTCCAGACTCACACACTCTG 21769
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                                                                                                         -----TTACTATCCACTCCTCAACGCCTTCAAGTCAACCTCCGGCAGCATG
                                                                                                                                                            GACGACCTCTACAACATGATGACGCGTCAAATCCGACTGTCCAAGACTCAACACTCCTG
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| CDS join(433 600,656 694,785 900,970 1078,1147 11375, 1434 1596,1662 1808,1874 2114,2194 2481) /gene="amy1" /EC number="3.2.1.1" /Codon start=1 /product="alpha-amy1ase" /procein_id="AAP14264.1" /db_xref="alpha-amy1ase" /bxsmlation="MMYAWWSLPLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTD GSTTATCNTADRKYCGTWGSIIDKLDYIQCNGFTA.WITPVTAQLPQTAYGDAYHG YWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVANHMGYDGAGSSVDYSVFKP FSSQDYFHPPCTIQNYSDGTYGDEDTALGTPVENYENEWPWGSLUYSN YSLDARATCKTAGRAGNDDLAALSOCHGDDAYTCPYQNVMDGSLUYSN YSLLNAFKSTSGSMDDLYNAINTVKSOCPDSTLGTPVENHDNRFRASYTNDIALAKN YAPLILNDGIPIIYAGGSNDDTANAINTVKSOCPDSTLGTPVENHDNRFRASYTNDIALAKN YARFIILNDGIPIIYAGGSNDPANREATWLGSTPVENHDRRFASYTNDIALAKN VAAFIILNDGIPIIYAGGSUDTANREATWLGSTPTDSLAKIIASNAIRNY AISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTIISNKGASGDSYTLSLSGAGYT AGGQLTTEVIGGTTTVTVGSDGNVPVPRAGGLBRVLYPFFEKLAGSKICSSS" | Query Match 56.9%; Score 985.8; DB 8; Length 2970; Best Local Similarity 74.6%; Pred: No. 1.6e-227; Indels 549; Gaps Matches 1616; Conservative 0; Mismatches 2; Indels 549; Gaps 1 TCACATCAAGCTCTCCTTCTCTGAACAATAAACCCCACAGAAGGCATTTATGATGGTCG 383 TCACATCAAGCTCTCTCTCTGAACAATAAAACCCCACAGAAGGCATTTATGATGGTCG 61 CGTGGTGGTCTTATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCAACGC 443 CGTGGTGGTCTTATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCAACGC | Qy 121 CTGCGGACTGGCGATCGATTATTACTTCTTCACGGATCGATTGCAAGGACGG 180 Db 503 CTGCGGACTGGCGATCGATTTATTACTTCCTTCTCACGGATCGATTTGCAAGGACGG 562 Qy 181 ATGGGTCGACGACTGCAATCGATTTATTACTTCCTTCTCACGGATTTGCAAGGACGG 562 Qy 181 ATGGGTCGACGACTGCAATCGAATCGCGATCGATTTGCAAGGACGT 622 Qy 217 AGGGTCGACGACTGCAATCGAGATCGGGATCGGATGGTATTGCTACTAGCTT 622 Qy 217 AGGGTCGACTGCACTTGATATACTGCGCTGTGTTGTTGCTACTAGCAGGC 245 Db 623 TCAGAAAGACGAATGTATAAAAATACTGTGGTGGAACATGGCAGGGC 682 Qy 246 ATCATCGACAAGGTAAAATGCCCCTTATCAAAAAAAAAA | Qy 256 |
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| | 1320 TCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCCTCTCC | QY 1500 TTGTATCCGACTGAGAAGTTGGCAGGTAGCAAGATCTGTAGTAGCTGGAAGGTGGAG 1559 Db 2597 TTGTATCCGACTGAGAGTTGGCAAGATCTGTAGTAGCTCGTAGGGTGGAG 2656 QY 1560 AGTATATCATCTGGCAATTGGCAAGTGAGTTTGAGTTTGAGTTTGAGTTTGATGTA 1618 Db 2657 AGTATATGATGGTATTCAATCTGGCATTGGAGTGAGTTTGATGTA 1618 AF139925 AF139925 2970 bp DNA linear PLN 01-DEC-1999 DEFINITION ASPESGILUS AF139925 2970 bp DNA linear PLN 01-DEC-1999 ACESSION AF139925 GI:6492298 GIIII GIII GIII GIII GIII GIII GIII GI | REFERENCE SOURCE ORGANISM Repergillus flavus ORGANISM Repergillus flavus ORGANISM Repergillus flavus ORGANISM Repergillus flavus Burdarydora, Fundi, Ascomycota, Pezizomycotina, Eurotiomycetes, Eurotiales; Trichocomaceae; mitosporic Trichocomaceae, Aspergillus. 1 (bases 1 to 2970) AUTHORS TITLE AMAI, the alpha-amylase gene of Aspergillus flavus: Involvement in aflatoxin biosyntheais in maize kernels JOURNAL PHYLOPACHOLOGY 89, 208-914 (1999) REFERENCE 2 (bases 1 to 2970) PEFFERENCE PAKHOURY, A. M. and Woloshuk, C.P. TITLE Direct Submission JOURNAL JOURN |

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YSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIY
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Aspergillus niger
Aspergillus niger
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 2443)
Korman,D.R. Bayliss,F.T., Barnett,C.C., Carmona,C.L., Kodama,K.H.,
Korman,D.R., Bayliss,F.T., Barnett,C.C., and Berka,R.M.
Cloning, characterization, and expression of two alpha-amylase
genes from Aspergillus niger var. awamori
Curr. Genet. 17 (3), 203-212 (1990)
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/mol type="genomic DNA"

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11. .13

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/gene="amyB"

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1103 TCGCGGATATGGTTCATTTCAGTACTGACAATGAGTAATATCAGGGCTATGATGGAGCGG 1162
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                                                      CACGTCCAGAAGGACTTCTGGCCCGGGTACAACAAAGCCGCAGGCGTGTACTGTATCGGC
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1 (bases 1 to 2520)

Korman, D.R., Bayliss, F.T., Barnett, C.C., Carmona, C.L., Kodama, K.H., Royer, T.J., Thompson, S.A., Ward, M., Wilson, L.J. and Berka, R.M. Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus niger var. awamori (curr. Genet. 17 (3), 203-212 (1990)
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1197. .1359,1425. .1571,1637. .1877,1957. .2238)
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/db_xref="taxon:5061"
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/note="1,4-alpha-D-glucan 4-glucanohydrolase"
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CCAGAAGGACTTCTGGCCCGGGTACAACAAGCCGCAGGCGTGTACTGTATCGGCGAGGT 1290
                                                                                                                                                                                                                                                                                1351 CTATCCCATGTATGGTTCCTCCAACCATGAGCCTTCTTGCAAGTCTCCATCTCCTAACGAA 1410
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                                                                                           GCTCGACGGTGATCCGTACACTTGTCCCTACCAGAACGTCATGGACGGCGTACTGAA
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| 256 | 511 TAAAATAAAAAGAACTCTAGTCCTAACCATCACATÄĞTTĞĞAČTATATCCAĞĞĞAATĞĞĞ 570 281 ÇTTCACAĞCCATCTĞĞATCAÇÇÇÇĞTTACAĞÇCCCAĞCTĞCCCCAĞACCAÇĞÇATATĞĞ 340 | 571 CTTCACAGCCATCTGGATCACCCCCGTTACAGCCCAGCTGCCCCAGACCACCCGCATATGG 630 | 341 AGATGCCTACCATGGCTACTGGCAGCAGGATT373 | | TGTCATCTTTTACATCAATATGAACTTAACTTGATGGTTTTTAGATACTCTCTGAACGAAAA | 392 CTACGGCACTGCAGATGACTTGAAGGCGCTCTTCGGCCCTTCATGAGAGGGGGATGTA 451 | 452 TCTTATGGTCGATGGTAACCATAT | | 571 GAIRIGGILCHIIICAGIACIGACARIGAGIAHRICAGACCIAIGAGACCAGAGACAGACAGACAGACAGACAG | | 564 ITCAITCAAAACTAIGAAGAICAGACTGAGGITGAGGAITGCTGGCTAGGAGAIAACACT 623 | 624 GTCTCCTTGCCTGATCTCGATACCACCAAGGATGTGGTCAAGAATGAAT | 684 GTGGGATCATTGGTATCGAACTACTCCA | TTGACGGCCTCCGTATCGACACAGTAAAACACGT | | CCAGAAGGACTTCTGGCCCGGGTACAAAGCCGCAGGCGTGTACTGTATCGGCGAGGT | GCTCGACGGTGATCCGGCCTACATCTTCCCTACCAGAACGTCATGGACGGCGTACTGAA | 866 CTATCCCAT | 875TTACTATCCACTCCTCAACGCCTTCAAGTCAACGCGGGGGGGG | 921 GACGACCTCTACAACATGATCAACGCCGTCAAATCCGACTGTCCAGACTCAACACTCTG 980 | 981 GGCACATTCGTCGAGAACCACGACAACCTCGCTTC |
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| /number=2 463. 547 /gene="amyA" | /number=2 548663 /gene="amyA" | /number=3 664732 /gene="mmvA" | /number=3 733841 /gene="amyA" | / Inducer= 4 842909 /gene="amyA" | /number=4 9101138 | /gene="mmyA" /number=5 /number=6 /number=6 | /gene="anyA" /number=5 11971359 /gene="amyA" | /number=6 1360. 1424 /gene="amyA" | / | /number=7 1572. 1636 1572. 1636 | /gene="anyA" /numbe="anyA" 16371877 /gene="amyA" | / Inducer=8 1878. 1956 / Gene="anyA" / number=8 | 19572241 John | 52.48; | 73.6%; Pred. No. 9.4e-209; ative 0; Mismatches 8; | TCACATCAAGCTCTCCCTTCTGAACAATAAACCCCACAGAAGGGATTTATGATGGTCG 60 | CGTGGTGGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCAÀCGC 120 | CTGCGGACTGGCGATCGCAATCCATTATTTCCTTCTCGGATCGATTTGCAAGGACGG 180 | | AGGGC | |
| intron | exon | intron | exon | intron | exon | intron | exon | intron | exon . | intron | exon | intron | exon polyA_site | Okicin Query Match | Best Local Similarity Matches 1537, Conserv | Qy 1 ' | Qy 61 0 | Qy 121 O | Oy 181 | 217 | |

| QY 68 GTCTCTATTTCTGTACGGCCTTCAGGTCGGGACCTGGGTTTTGGCTGCTACGCCTGCGGA 127 Db 3 GACAATCTTTCTGTTTCTGGCCATTTTCGTGGCTACAGCTCTGGCACGCCTGCAGGCAG | Qy 128 CTGGCGATCGCAATCCATTATTTCCTTCTCACGGATCGATTTGCAAGGACGGATGGTC 187 | Oy 188 GACGACTGCGACTTGTAATACTGCGGATCAGAATACTGTGGTGGAACATGGCAGGCA | QY 248 CATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGCCATCTGGATCACCCCGT 307 | QY 308 TACAGCCCAGCTGCCCCAGACCACGCATATGGAGATGCTACCATGGCTACTGGCAGCA 367 Db 243 AACTGCACGAATACTGGTTACGGATATCAGGATACTGGAGCA 302 | Qy 368 GGATATACTCTCTGAACGAAACTACGGCACTGCAGATGACTTGAAGGCGCTCTTTC 427 | QY 428 GGCCCTTCATGAGAGGGGATGTATCTTATGGTCGATGTGGTTGCTAACCATATGGGCTA 487 | QY 488 TGATGGAGCGGGTAGCTCCAGTCGATTACAGTGTTTAAACCGTTCAGTTCCCAAGACTA 547 | OY 548 CITCCACCGTTCTGTTTCATACAAACTATGAAGATCAGATTGAGGATTGCTG 607 | QY 608 GCTAGGAGATAACACTGTCTCTTGCCTGATCTCGATACCACAGGATGTGGTCAAGAA 667 | Qy 668 TGAALGGTACGACTGGGATCATTGGTATCGAACTACTCCATTGACGGCCTCCGTAT 727 Db 603 TATGTGGTATGACTGGGTCGAGTCTCTGTCTAACTACTGCGTCGACGCCTCCGCGT 662 | Qy 728 CGACACAGTAAAACACGTCCAGAAGGACTTCTGGCCCGGGTACAAAGCCGCAGGCGT 787 | 848 CAIGGACGCCTACTGAACTAICCCAITTACTAICCACTCCTCAACGCCTICAAGTCAAC | | Qy 968 CTCAACACTCCTGGGCACATTCGTCGAGAACCACGACGGTTCGCTTCTTA 102 | Qy 1025 CACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCATCATCAGACGACGAAT 1084 Db 963 CACAAGCGACATGTCCCTAGCCAAAAATGCCGCAACATTCACTATCCTGGCTGACGCCAT 1022 | Oy 1085 CCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGGGGAAACGGCCCGCGAAACG 1144 |
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| Oy 1022TTACACCAACGACA 1035 Db 1591 TTCCGTTCCACACACACACACCCACCTAACAAGAGCAAAGTTACACCAACGACA 1650 | Qy 1036 TAGCCCTCGCCAAGAACGTCGCAGCATTCATCCTCAACGACGGAATCCCCATCATCT 1095 | OY 1096 ACGCCGGCCAAGAACAGCACTACGCCGGGAAACGAACGCTCGCGAACCT 1155 | Qy 1156 GGCTCTCGGGCTACCGACAGCGAGTGTACAAGTTAATTGCCTCGGGAACGCAA 1215 Db 1771 GGCTCTCGGGCTACCCGACCGACGGGGTGTACAAGTTAATTGCCTCCCGGAACGCAA 1830 | Qy 1216 TCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA 1260 | Qy 1261 | OY 1261AGAACTGGCCCATCTACAAAGACGACAACGATGGCCATGGGCAAGGGCACAGAT 1316 | Qy 1317 GGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCTC 1376 D 2011 GGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCTC 2070 | QY 1377 TCCTTGAGTGGTGGTACACAGCCGGCCAGCAATTGACGGAGGTCATTGGCTGCACG 1436 DD 2071 TCCTTGAGTGGTGCGGGTTACACAGCCGGCCAGCAATTGACGGAGGTCATTGGCTGCACG 2130 | QY 1437 ACCGIGACGGTTGGTTCGANGAAATGTGCCTGTTCCTANGGCAGGTGGCTACCTAGG 1496 Db 2131 ACCGTGACGGTTGGTTCGGANGGAAATGTGCCTGTTCCTANGGCAGGTGGCTACCTACGG 2190 | OY 1497 GTATTGTATCCGACTGAGAAGTTGGCAGGTAGCAAGATCTGTAGTAGCT 1545 | RESULT 15 AX711606 LOCUS AX711606 AX711606 AX711606 AX711606 AX711606 ACCESSION AX711606 ACCESSION AX711606 AX711606 AX711606 ACCESSION AX711606 AX711606 AX711606 AX711606 AX711606 AX711606 AX711606 AX711606 AX711606 AX711606 AX711606 | _ | 1 Maier,D., Stock,A., Wagner,C., Folkers,U., Albermann,K. Hopper,S. Novel amylases and uses thereof | JOURNAL Patent: WO 03016535-A 7 27-FEB-2003; DSM N.V. (NL) FEATURES 1 | | ORIGIN Query Match 43.8%; Score 759.8; DB 6; Length 1485; Best Local Similarity 70.0%; Pred. No. 7.38-173; Matches 1038; Conservative 0; Mismatches 442; Indels 3; Gaps 1; |

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1265 CTGGCCCATCTACAAAGACGACACAATCGCCATGCGCAAGGGCACAGATGGGTCGCA 1324
1203 CTACCCCATCTACCAAGACACCTCGACCTTGCCATGGCGCAAAGGCTACAATGGCACCCA 1262
                                                                                                                                                           1385 TGGTGCGGGTTACACAGCGGCCAGCAATTGACGGAGGTCATTGGCTGCACGACCGTGAC 1444
1323 AGGAACAGGCTACACACGCCGAAAGATTACTGAAATCTATACCTGCACGAATCTAAC 1382
1083 CGAAGCGACCTGGCTTTCAGGCTACAAGACCACCAGGGGGGGTCTACACCCATATCGCGGC 1142
                                                                                                                                                                                                                                                                                                 1205 GGCGAACGCAATCCGGAACTATGCCATTAGCAAGATACAGGATTCGTGACCTACAAGAA 1264
                                                               1143 ATCGAACAAGATTCGCACCCACGCTATAAAACAGGATACCGGATATCTCACCTACAAAAA 1202
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Search completed: February 11, 2005, 21:34:13 Job time : 7426 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on:

February 11, 2005, 14:14:01; Search time 906 Seconds · (without alignments) 11329.836 Million cell updates/sec

US-10-820-200-1

Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* 1: geneseqn1980s:* Database

geneseqn1990s:* geneseqn1980s:

geneseqn2003cs:* geneseqn2003ds:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2000s:* geneseqn2001as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004as:*geneseqn2004bs:*

| ВS | Description | Aaf90208 Nucleotid | Aaf12832 Aspergill | Aag06786 Taka-amyl | Acc44572 Alpha-amy | Adt89627 Appergil | Adt89631 Aspergil | Aaf11252 Aspergill | Abq80346 A. fumiga | Acc43088 Nucleotid | Abg80348 A. fumiga | Aaq88712 Aspergill | | Aag25079 Alpha-amy | | Aag77665 Variant a | | Aaf11314 Aspergill | | Aag77667 Variant a | Aag06388 AMY1 gene |
|-----------|-----------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|----------|--------------------|------------|--------------------|--------------------|
| SUMMARIES | a a | AAF90208 | AAF12832 | AAQ06786 | ACC44572 | ADT89627 | ADT89631 | AAF11252 | ABQ80346 | ACC43088 | ABQ80348 | AAQ88712 | AAF11252 | AAQ25079 | AAN70916 | AAQ77665 | AAQ77668 | AAF11314 | AAQ77666 . | AAQ77667 | AAQ06388 |
| | 8 | 4 | e | ~ | œ | 13 | 13 | ო | 10 | æ | 10 | N | m | N | Н | 0 | ~ | m | 0 | 7 | ~ |
| | Match Length DB | 1734 | 1914 | 2337 | 3285 | 2443 | 2520 | 1389 | 1488 | 1485 | 1893 | 1956 | 1389 | 1404 | 4214 | 1404 | 1404 | 483 | 1404 | 1404 | 2289 |
| Query | Match | 100.0 | 98.4 | 61.3 | 58.3 | 56.5 | 52.4 | 46.5 | 45.3 | 43.8 | 37.4 | 32.9 | 25.3 | 21.8 | 21.8 | 21.6 | 21.6 | 21.6 | 21.6 | 21.6 | 21.3 |
| | Score | 1734 | 1707 | 1063.8 | 1011.2 | 979 | 908.2 | 908 | 786 | 759.8 | 648.2 | 570 | 439 | 378.6 | 377.4 | 375.4 | 375.4 | 374.2 | 373.8 | 373.8 | 369.2 |
| Result | No. | - | 8 | m | 4 | ι. | 9 | 7 | ۵ | 0, | 10 | נו | c 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 |

New variant of Fungamyl-like alpha-amylase, useful for production of maltose syrups, includes mutations that improve stability against heat and acidic pH.

| Abt14461 HCV envel Aad50611 pMF30 vec Abd84219 Vector pM Aaf11273 Aspergill Aan81525 Sequence Aan81525 Sequence Aan8177 5, end of Aaf11253 Aspergill Acc43090 Nucleotid Abd80345 A. fumiga Abd80345 A. fumiga Acc43081 Nucleotid Acc43084 Nucleotid Acc43084 Nucleotid Acc43089 Nucleotid Abg80347 A. fumiga Abg80347 A. fumiga Abg80348 Aspergill Acc43083 Nucleotid Abg80380 Nucleotid Abg80380 A. fumiga Abg80349 A. fumiga |
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ALIGNMENTS

Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose; alcohol; starch; dough improver; brewing; starch liquification; ss. Location/Qualifiers 54. .1550 /*tag= a /product= "fungamyl-like alpha-amylase" Nucleotide sequence of a fungamyl-like alpha-amylase. Svendsen A, Pedersen S; AAF90208 standard; DNA; 1734 BP. 10-NOV-2000; 2000WO-DK000626. 99DK-00001617 54. .113 /*tag= b 114. .1547 /*tag= c (first entry) (NOVO) NOVOZYMES AS Bisgard-Frantzen H, WPI; 2001-367478/38. P-PSDB; AAB84206. Aspergillus oryzae. WO200134784-A1 10-NOV-1999; 17-MAY-2001. 06-AUG-2001 sig_peptide mat_peptide AAF90208; Key RESULT 1

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                   The present sequence encodes a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, which have an alteration in one the amino acid regions 98-110, 150-160, 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic pH, relative to wild-type enzyme. The variants can therefore be used at higher temperatures (more efficient conversion or faster reaction, and have reduced need for cooling and reduced risk of contamination). The variants may also be used in conjunction with other enzymes, particularly glucoamylase during dextrinisation. The variants are used to produce syrups, particularly of high maltose content, or alcohol, from starch; as dough improver for baked goods; in brewing, to increase fermentability of the wort, and for liquefaction of starch
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1734; Conservative 0; Mismatches
 Page 40-42; 49pp; English
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Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.
                                             Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; se.
                                                                                                                                                                                                                                                                                                             88; Page 2231-2232; 3161pp; English
                             Aspergillus oryzae EST SEQ ID NO:5355
                                                                                                                                                                                                     (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the retail of the same genes in one or more second filamentous fungal cells. The methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the same genes in one or more second filamentous fungal cells. Monitoring the cap global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered; cossible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of gene copy number variation and stability can be monitored. The expression of gene copy number variation and stability can be monitored. The expression of gene copy number variation and stability can be monitored. The expression of gene copy number variation and stability can be monitored. The expression of dentabolic or catabolic pathway engineering. Using ESTB provides several cavantages over genomic or random cDNA clones including elimination of redundancy as one apot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene copy reducts to facilitate analysis of the results. ARF01481 to AAF11487 copy from the free copy from Aspergillus niger; AAF1187 to AAF14878 tepresents ESTS from Fusarium venenatum; ABF11878 represents ESTS from Fusarium venenatum; ABF11878 represents ESTS from Fusarium venenatum; ABF11871 to Fusariand in the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatum of the venenatu Trichoderma reesei, which are all specifically claimed in the present

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1080 1200 1020 1022 1082 1201 CCTCCGCGAACGCAATCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA 1260 482 960 240 242 300 360 420 480 540 542 900 602 99 662 720 722 780 782 840 900 902 962 182 302 362 422 842 423 TCTCTTCGGCCCTTCATGAGAGGGGATGTATCTTATGGTCGATGTGGTTGCTAACCATA 123 CTGCGGACTGGCGATCGCAATCCATTATTTCCTTCTCACGGATCGATTTGCAAGGACGG 183 ATGGGTCGACGACGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGAACATGGC AGGCATCATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGGCATCTGGATCA TCCGTATCGACACAGTAAAACACGTCCAGAAGGACTTCTGGCCCGGGTACAAAGCCG GTCCAGACTCAACACTCCTGGGCACATTCGTCGAGAACCACGACAACCCACGGTTCGCTT GTCCAGACTCAACACTCCTGGGCACATTCGTCGAGAACCACGGACAACCCACGGTTCGCTT CTTACACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACG GAATCCCCATCATCTAGGCCGGCCAAGAACAGCACTACGCCGGGAAACGACCCCGCGA AGGGCATCATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGCCATCTGGATCA CCCCCGTTACAGCCCAGCTGCCCCAGACCACCGCATATGGAGATGCCTACCATGGCTACT CCCCCGTTACAGCCCCAGCTGCCCCAGACCACCGCATATGGAGATGCCTACCATGGCTACT GGCAGCAGGATATATATCTCTCTGAACGAAAACTACGGCACTGCAGATGACTTGAAGGCGC GGCAGCAGGATATATATACTCTCTGAACGAAAACTACGGCACTGCAGATGACTTGAAGGCGC TCTCTTCGGCCCTTCATGAGAGGGGATGTATCTTATGGTCGATGTGGTTGCTAACCATA TGGGCTATGATGGAGCGGGTAGCTCAGTCGATTACAGTGTTTAAAACCGTTCAGTTCCC 541 AAGACTACTTCCACCCGTTCTGTTTCAAAACTATGAAGATCAGACTCAGGTTGAGG 543 AAGACTACTTCCACCCGTTCTGTTTCATTCAAAACTATGAAGATCAGACTCAGGTTGAGG ATTGCTGGCTAGGAGATAACACTGTCTTGCCTGATCTCGATACCACCAAGGATGTGG 603 ATTGCTGGCTAGGAGATAACACTGTCTCCTTGCCTGATCTCGATACCACCAAGGATGTGG TCAAGAATGAATGGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATTGACGGCC TCCGTATCGACACAGTAAAACACGTCCAGAAGGACTTCTGGCCCGGGTACAAAGCCG CAGGCGTGTACTGTATCGGCGAGGTGCTCGACGGTGATCCGGCCTACACTTGTCCCTACC AGAACGTCATGGACGGCGTACTGAACTATCCCATTTACTATCCACTCCTCAACGCCTTCA AGTCAACCTCCGGCAGCATGGACGACCTCTACAACATGATCAACACGCGTCAAATCCGACT AGTCAACCTCCGGCAGCATGGACGACCTCTACAACATGATCAACACGCCGTCAAATCCGACT CTTACACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCTCTCAACGACG 1083 GAATCCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGCGGAAACGACCCCGCGA **ACCGCGAAGCAACCTGGCTCTCGGGCTACCCGACCGACAGCGAGCTGTACAAGTTAATTG** Acceceaaecaaccidecreteceeeracceaacaecaecaecaerarararre **ATGGGTCGACGACTGCGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGAACATGGC** 243 723 843 903 1081 1143 421 1021 1141 241 301 303 361 363 481 483 783 841 901 1023 121 181 601 661 721 781 961 963 요 셤 8 셤 셤 셤 셤 유 요 셤 셤 셤 셤 8 셤 ò ò 셤 8 ò ò ò à ò 셤 ò ò 셤 ò ò ò 8 ઠ ò

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                                    Length 2337;
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                                      DB 2;
                                     61.3%; Score 1063.8; DB 2; 75.3%; Pred. No. 4.7e-235; iive 0; Mismatches 7;
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                   Sequence 2337 BP; 630 A; 600 C; 533 G;
24-OCT-2003 to standardise OS field)
                                               Best Local Similarity 75.3
Matches 1700; Conservative
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CCTCCGCGAACGCAATCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA
                                      1263 AGAACTGGCCCATCTACAAAGACGACACAACGATGCCCATGCGCAAGGGCACAGATGGGT
                                                                             CGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCCTCTCCT
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                                                                   CGCAGATCGTGACTATCTTGTCCAACAAGGTGCTTCGGGTGATTCGTATACCCTCTCCT
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The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose isomerase, or glucosmylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act upon the desired substrate. Also described are self-processing transgenic plants and plant parts, e.g. grain, which express one or more of these enzymes and have an altered composition that facilitates plant and grain processing. Also described is a method (N) for converting starch to starch-derived products in a transformed plant part (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful for preparing maltodextrin. A transformed plant (TP) can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
                                                                                                                                                                                                                                                                                                                                                                                    Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucoardase; glucoardase; glucoardase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme; gene; se.
                                                                                                                2228 GITIGARGIACAGITIGAGAGICGITACIGCIGICAICCCCITATATACICGITIGITITIT
   2108 TACCTAGGGTATTGTATCCGACTGAGAAGTTGGCAGGTAGCAAGATCTGTAGTAGCTCGT
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|/ttag= a
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|product= "alpha-amylase/glucoamylase fusion protein"
/note= "no start or stop codons given"
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produce food products having improved taste and to produce fermentable substrates for ethanol and fermented beverages. (M) eliminates the need to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence encodes alpha-amylase/glucoamylase fusion protein, which is given in the exemplification of the present invention
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Pred. No. 6.8e-223;
0; Mismatches 258; Indels
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Best Local Similarity 81.9%;
Matches 1166; Conservative
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Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological

Example 10; SEQ ID NO 17; 58pp; English

The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger et, and medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance and second nucleotide heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) gene.

270 180 330 390 340 630 373 810 870 930 210 120 216 245 255 510 280 570 690 750 503 450 391 451 481 9 CGTGGTGGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCAACGC CTTCACAGCCATCTGGATCACCCCCGTTACAGCCCCAGCTGCCCCAGACCACCACATATGG TCACATCAAGCTCTCCCTTCTCGAACAATAAACCCCACAGAAGGCATTTATGATGGTCG CTGCGGACTGGCGATCGCAATCCATTAATTTCCTTCTCACGGATCGATTTGCAAGGACGG CTGCGGACTGGCGATCGCAATCCATTATTTCCTTCTCACGGATCGATTTGCAAGGACGG --------CTTCACAGCCCATCTGGATCACCCCCGTTACAGCCCAGCTGCCCCAGACCACCGCATATGG AGATGCCTACCATGCCTACTGGCAGCAGGATATGTAAGTCGATTTCTTTAAATATCTACC ----ATACTCTCTGAACGAAAA CTACGGCACTGCAGATGACTTGAAGGCGCTCTTCGGCCCCTTCATGAGAGGGGGATGTA cracescacrecaeareacrreaaeeeecrcrcrceeeecrrcareaeeeeearera CTGAACAATAAACCCCACAGAAGGCATTTATGATGGTCG CGTGGTGGTCTCTATTTCTGTACGGCCTTCAGGTCGCGCGCACCTGCTTTGGCTGCAACGC ----AGAAATACTGTGGTGGAACATGGCAGGGC -----AGTIGGACTATATCCAGGGAATGGG ------GGGCTATGATGGGGCGGTAGC Gaps 544; Length 2443; Sequence 2443 BP; 669 A; 620 C; 558 G; 595 T; 0 U; 1 Other; Score 979; DB 13; Length 24 Pred. No. 1.7e-215; 0; Mismatches 10; Indels ATGGGTCGACGACTGCGACTTGTAATACTGCGGATC-----AGATGCCTACCATGGCTACTGGCAGCAGGATAT-TCACATCAAGCTCTCCCTTCT Query Match
Best Local Similarity 74.4%;
Matches 1609; Conservative ATCATCGACA-246 211 217 391 451 256 511 571 341 631 691 751 452 811 482 151 19 121 271 181 331 281 374 392

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| δ d d | 504 | TCAGTCGATTACAGTGTTTAAACCGTTCAGTTCCCAAGACTACTTCCACCGTTCTGT 5: | 563 |
|-------------|------|--|------|
| ò | 564 | TTCATTCAAAACTATGAAGATCAGACTCAGGTTGAGGATTGCTGGCTAGGAGATAACACT 6 | 623 |
| qa | 991 | TTCATTCAAAACTATGAAGATCAGACTCAGGTTGAGGATTGCTGGCTAGGAGATAACACT 1 | 020 |
| à à | 624 | 224 GTCTCCTTGCCTGATCTCGATACCACGAGGATGTGGTCAAGAATGAAT | |
| o o | 1051 | GTCTCCTTGCCTGATCTCGATACCACCAAGGATGTGATGAATGA | 011 |
| ે ઇ | 684 | GTGGGATCATTGGTATCGAACTACTCCA | |
| a 8 | 713 | GIGGGAICATIGGIAICGAACIACICCAGIAAGAIAITICICCCICAIICIACAAAAALITGG 1. | 170 |
| · 음 음 | 1171 | CTGATCGATGATACTTACGAAATCAGTTGACGGCCTCCGTATCGACAGTAAAACACGT 1: | 230 |
| ò | 746 | CCAGAAGGACTTCTGGCCCGGGTACAAAGCCGCAGGCGTGTACTGTATCGGCGAGGT 80 | 0.5 |
| op. | 1231 | CCAGAAGGACTTCTGGCCCGGGTACAAAAGCCGCAGGCGTGTACTGTATCGGCGAGGT 1. | 290 |
| ò | 806 | 106 GCTCGACGGGAATCCGGCCTACACTTGTCCCTACCAGAAGGTCATGGACGGCGTACTGAA 865 | 9 |
| Ор | 1291 | GCTCGACGGTGATCCGGCCTACACTTGTCCCTACCAGAACGTCATGGACGGCGTACTGAA 1. | 1350 |
| λ | 998 | CTATCCCAT | 74 |
| Db | 1351 | CIAICCCAIGTAIGGIICCICCAACCAIGAGCCIICIIGCAAGICICAICICCIAACGAA 1. | 410 |
| ò | 875 | TTACTATCCACTCCTCAACGCCTTCAAGTCAACCTCCGGCAGCATG 9 | 20 |
| qq | 1411 | ACGGCTAAAACCAGTTACTATCCACTCCTCAACGCCTTCAAGTCAACCTCCGGCAGCATG 1. | 470 |
| ò | 921 | GACGACCTCTACAACATGATCACCGTCAAATCCGACTGTCCAGACTCAACACTCCTG 9 | 80 |
| QQ | 1471 | GACGACCTCTACAACATGATCAACACGTCAAATCCGACTGTCCAGACTCAACACCCCTG 1 | 530 |
| ò | 981 | GGCACATTCGTCGAGAACCACGACAACCCACGGTTCGCTTC | 021 |
| qq | 1531 | GGCACATTCGTCGAGAACCACGACACCCACGGTTCGCTACGTAAGTCTTCCCTTTATT 1. | |
| ò | 1022 | 022TTACACCAACGACA 103 | 035 |
| QQ | 1591 | TTCCGTTCCCAATTTCCACACAGAACCCCACCTAACAAGAGCAAAGGTTACACCAACGACA 1 | |
| à | 1036 | TAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCTCAACGACGGAATCCCCATCATCT 1 | 1095 |
| Dp | 1651 | TAGCCCTCGCCAAGAACGTCGCAGCATTCATCTCCTCAACGACGGAATCCCCATCATCT 1. | |
| ò | 1096 | ACGCCGGCCAAGAACAGCACTACGCCGGCGGAAACGACCCCCGCGAACGCGAAGCAACCT 1. | |
| QQ | 1711 | ACGCCGGCCAAGAACAGCACTACGCCGGCGAAACGACCCCGCGAACCGCGAAGCAACCT 1. | - |
| ò | 1156 | 156 GGCTCTCGGGCTACCCGACCGACGCGAGCTGTACAGTTAATTGCCTCCGCGAACGCAA 121 | 1215 |
| qq | 1771 | decreredectacedacedacedacederadataaridecreecedaacedaa 10 | 830 |
| <i>λ</i> ο | 1216 | TCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA 1: | 260 |
| qq | 1831 | TCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACAAGGTAAGCACAACCT 1 | 1890 |
| ò | 1261 | 1 | 260 |
| QQ | 1891 | CTAAGCATACCCTAATGGCCTATCTTCAGAGTATCTGACACAAGAGACTAATCACTGGCA 1. | 950 |
| δ | 1261 | AGAACTGGCCCATCTACAAAGACGACACAACGATGCCCATGCGCAAGGCACAGAT 1. | |
| qq | 1951 | ATACAGAACTGGCCCATCTACAAAGACGACAACGATCCCGGATGCGCAAGGGCACAGAT 20 | 010 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 TCAGAAAGAGGAATGTAAACTGACTTGATATAGAAATACTGTGGTGGAACATGGCAGGG
                                   The present sequence is the
sequences comprising modification of glucoamylase (glaA) and heterologous biological substance. The present sequence is th Aspergillus niger neutral alpha-amylase A (amyA) gene.
                                                                                                               Sequence 2520 BP; 682 A; 645 C; 581 G; 611 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
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                                                                                                                                                                      Score 908.2; DB 1.
Pred. No. 3.5e-199
0; Mismatches 8
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                                                                                                                                                                Query Match 52.4%;
Best Local Similarity 73.6%;
Matches 1537; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATTGTATCCGACTGAGGAAGTTGGCAGGTAGCAAGATCTGTAGTAGCTCGTGAAGGCTG
     GGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCCTC
                                              GGGTCGCAGATCGTGACTATCTTGTCCAACAAGGTGCTTCGGGTGATTCGTATACCCTC
                                                                                                                 TCCTTGAGTGGGGGTTACACAGCCGGCCAGCAATTGACGGAGGTCATTGGCTGCACG
                                                                                                                                                       TCCTTGAGTGGTGCGGGTTACACAGCCGGCCAGCAATTGACGGAGGTCATTGGCTGCACG
                                                                                                                                                                                                                                   ACCGTGACGGTTGGTTCGGATGGAAATGTGCCTGTTCCTATGGCAGGTGGGCTACCTAGG
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201. .2244
/*tag= a
//*toduct="Neutral alpha-amylase A (amyA) protein"
/note= "CDS has many translational exceptions which alters the reading frame"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucoamylase; glaA; amyA; alpha-amylase A;
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P-PSDB; ADT89632.
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1497 GTATTGTATCCGACTGAGAAGTTGGCAGGTAGCAAGATCTGTAGTAGCT
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expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma resea!; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; se Multiple gene expression; filamentous fungal cell; EST; Aspergillus niger EST SEQ ID NO:3775. AAF11252 standard; cDNA; 1389 (first entry) 13-MAR-2001 AAF11252; RESULT 요

(NOVO) NOVO NORDISK BIOTECH INC. (NOVO) NOVO NORDISK AS. 22-MAR-2000; 2000WO-US007781. Aspergillus niger. WO200056762-A2. 22-MAR-1999; 28-SEP-2000

Olsen PB; Clausen IG, Kauppinen S, Shuster JR, WPI; 2000-594572/56. Berka RM, Rey MW,

Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.

Claim 87; Page 1694-1695; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the method uses fluorescence-labeled nucleic acids isolated from the methods for monitoring differential expression of genes are used in the methods for monitoring differential expression of the same genes in one or more second filamentous fungal cells. Monitoring the same genes in one or more second filamentous fungal cells. Monitoring the came genes in one or more second filamentous fungal cells. Monitoring the companions to be improved. New genes may be discovered, or feem microorapanisms to be improved. New genes may be discovered, or gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTS provides several advantages over genomic or random CDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene cop products to facilitate analysis of the results. AAF0148 to AAF11247

CE PEPESETS from Aspergillus niger; AAF11854 to AAF11248 to AAF11253 represents ESTS from Aspergillus niger; AAF11854 to AAF18537 represents ESTS from Aspergillus niger; AAF11854 to AAF1851 represents considered to the present considered to the present considered to the consideration of the gene considered to the considered to the present considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the considered to the

Sequence 1389 BP; 354 A; 384 C; 325 G; 326 T; 0 U; 0 Other;

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ABQ80346 standard; cDNA; 1488 BP 11-AUG-2003 (first entry) A. fumigatus AfAAL1 cDNA. ABQ80346; RESULT 8 ABQ80346 ZZZZZZZZZZZZZ ZZZZZZZZZZZZZZZ

Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase; beta-galactosidase; invertase; lipse; alpha-amylase; laccase; bolygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;

polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability; ss. glyceride; starch; maltodextrin; oxidated phenolic compound;

Aspergillus fumigatus.

/product= "Alpha amylase 1" ocation/Qualifiers 1. .1488 /*tag= a

WO2003012071-A2

13-FEB-2003

05-AUG-2002; 2002WO-US024842.

03-AUG-2001; 2001US-0309870P.

(ELIT-) ELITRA PHARM INC.

Bussey H; Roemer T, Jiang B, Storms R,

WPI; 2003-332729/31. P-PSDB; ABB80177.

Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.

Claim 2; Page 132-34; 169pp; English.

The sequences given in ABG80119-66 encode enzymatic proteins derived from C. A. funigatus. The resulting proteins display the catalytic activity of an enzyme such as tannase, cellulase, glucose oxidase, glucoamylase, phytase that a tannase are polygalaturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of compositions comprising dallate are useful for modulating the amount of cellulose in a composition. Compositions comprising the amount of glucose oxidase are useful for modulating the amount of cellulose in a composition composition of myo-inosical phosphates of a composition. Compositions comprising plucose oxidase are useful for modulating the amount of accessing phytase are useful for modulating the amount of lactose in a composition. Compositions comprising phytase are useful for modulating the amount of lactose in a composition composition composition composition composition composition in a composition of access are useful for modulating the amount of glyceride in a composition composition comprising alpha-amylases are useful for modulating the amount of glyceride in a composition composition comprising comprising in a composition. Compositions comprising comprising in a composition comprising phytalacturonases are useful for modulating the amount of xylan or xylo-oligomers are useful for modulating the amount of xylan or xylo-oligomers computation. The composition composition composition composition composition composition comprising plygalacturonic acid chains in a composition for modulating the amount of xylan or xylo-oligomers composition. The composition co

Sequence 1488 BP; 364 A; 410 C; 358 G; 356 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes an alpha-amylase enzyme of the filamentous fungus Aspergillus niger. Alpha-amylases catalyse the endohydrolysis of
                                                              11.78 GCAAGGACCCGGGATACGTGACTTATAAGAATAACCCCATCTACAAGATACCTCCACCA
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                <u> ATTACAGCGGCGCGGATCCCGCAAACCGTGAGGCAGTCTGGCTATCCGGCTACTCGA</u>
                                             CCGACAGCGAGCTGTACAAGTTAATTGCCTCCGCGAACGCAATCCGGAACTATGCCATTA
                                                                                                     GCAAAGATACAGGATTCGTGACCTACAAGAACTGGCCCATCTACAAAGACGACACAAGGA
                                                                                                                                                               TCGCCATGCGCAAGGGCACAGATGGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTG
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 Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosídic linkage; oligosaccharide; polysaccharide; baking; ss.
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16-AUG-2001; 2001EP-00000380.
16-AUG-2001; 2001EP-00000381.
16-AUG-2001; 2001EP-00000382.
16-AUG-2001; 2001EP-00000383.
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Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase; beta-galactosidase; invertase; lipase; alpha-amylase; laccase; bolygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; plyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylan; teod; feed; beverage; textile; tea liquor; cleaning ability; ss.
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                                    963 CACAAGGGACATGTCCCTAGCCAAAATGCCGCAACATTCACTATCCTGGCTGACGGTT
                                                                        CCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGGGGAAACGACCCCGGGGAACCG
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                CACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACGGAAT
                                                                                                                                   CGAAGCAACCTGGCTCTCGGGCTACCCGACCGACGCGAGCTGTACAAGTTAATTGCCTC
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1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. The alpha-amylase polynucleotides and polypeptides of the invention are
                                                                                                                                                                                                                            ATGGCGCTCCCAGTCGATATTTCCTGCTCACCGATCGCTTTGCGCGAACGGATAATTC
                                                                                                                                                                                                                                                                                    123 TACCACTGCTTCTTGTGACTTGAGCGCTCGGCAATATTGCGGTGGATCCTGGCAGGGCAT
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Pred. No. 4.9e-165;
0; Mismatches 442; Indels
                                                                                                                                                GTCTCTATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCT
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Bussey H; Roemer T, Storms R,

WPI; 2003-332729/31. P-PSDB; ABB80178.

Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.

Claim 2; Page 136-39; 169pp; English

The sequences given in ABQB0119-66 encode enzymatic proteins derived from Car funigatus. The resulting proteins display the catalytic activity of an enzyme such as tannase, cellulase glucose oxidase julocamylase, laccase, phytase, beta-galactosidases, invertase, lipase, alpha amylase, laccase, phytase, beta-galactosidases, invertase, lipase, alpha amylase, laccase, polygalacturomase or xylanase. Compositions comprising cellulase are useful for modulating the amount of cellulose in a composition comprising galucose oxidase are useful for modulating the amount of cellulose in a composition comprising galucose oxidase are useful for modulating the amount of compositions comprising phytase are useful for modulating the amount of lactose in a composition. Compositions comprising phytase are useful for modulating the amount of lactose in a composition. Composition comprising during the amount of glyceride in a composition. Composition comprising comprising altonates are useful for modulating the amount of glyceride in a composition. Composition comprising comprising comprising comprising comprising comprising comprising comprising comprising comprising comprising comprising composition. Compositions comprising polygalacturohases are useful for modulating the amount of xylan or xylo-oligomer of starches or malcodaxtrins in a composition. Compositions comprising polygalacturohases are useful for modulating the amount of xylan or xylo-oligomer composition. The modulating the amount of xylan or xylo-oligomer composition. The modulating the amount of xylan or xylo-oligomer composition or composition composition or compositio

Sequence 1893 BP; 425 A; 568 C; 475 G; 425 T; 0 U; 0 Other;

208 TATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCAACGCCTGCGGACTGGC 132 148 312 268 GATCGCAATCCATTTATTTCCTTCTCACGGATCGATTTGCAAGGACGGATGGGTCGACGA 192 CTGCGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGAACATGGCAGGGCATCATCG 252 313 CCCAGCTGCCCCAGACCACCGCATATGGAGATGCCTACCATGGCTACTGGCAGCAGGATA 372 88 crecreceargreacearcacearcacreratices ACAAGTTGGACTATATCCAGGGAATGGCCTTCACAGCCATCTGGATCACCCCCCGTTACAG ATCATCTCGACTACATTCAAGGCATGGGATTTACTGCCATATGGATCACCCCCGTAACTG rerccrerercercerecresacasseriseceanserersacecasses GCAGTCAATCGATCTATTTCCTCTGACCGATCGGTTCGGCCGAGAAGACAATTCCACGA Gaps Length 1893; ñ Indels Score 648.2; DB 10; Pred. No. 2.8e-139; 0; Mismatches 508; 1 37.4%; Query Match Best Local Similarity 65.4 Matches 966; Conservative 73 53 133 89 149 193 253 g 셤 셤 ò 요

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                    TCAGCGGAGGCGGCTACACGTCCGGCACGAAGCTCATCGAAGCGTACACCTGCACGTCCG 1330
                                                                                  1331 TGACGGTGGACTCGAACGGGGATATCCCTGTGCCGATGGCTTCGGGATTACCTAGAGTTC 1390
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                                                                                                                                                                                                                                                                                                                                                                                           Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; se.
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Kauppinen S,
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polymerisation; DP; transglycosifier; ss.
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Trichoderma reesei, which are all specifically claimed in the present
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                                                                                                                                                                               Sequence 1389 BP; 354 A; 384 C; 325 G; 326 T; 0 U; 0 Other;
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CTTACACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCTCAACGACG
                                                                                                                                       GICCAGACTCAACACTCCTGGGCACATTCGTCGAGAACCACGACAACCCACGGTTCGCTT
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                                                                                                                                                                       The variant alpha amylase gene was obtd. by mutating the 329th nucleotide of the alpha amylase gene of Saccharomycopsis fibuligera to T. This mutation results in substitution of the wild-type amino acid at position 84 of alpha-amylase by leucine. The variant alpha-amylase is high in transglycosifying activity. The variant alpha-amylase may be used to prepare malto-oligosaccharides with a degree of polymerisation (DP) of at least 7, by inversion of the malto-oligosaccharide. (Updated on 25-MAR-2003 to correct PA field.)
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                                                           Variant alpha-amylase gene for mfr. of malto-oligosaccharide(s) - is obtd. by mutating the nucleotide at position 329 of the Saccharomycopsis fibuligera wild type sequence to thymine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAGAATGAATGGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATTGACGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                          Score 378.6; DB 2; Length 1404;
Pred. No. 3.6e-77;
0; Mismatches 584; Indels 15;
                                                                                                                                                                                                                                                                                                                                                      Sequence 1404 BP; 407 A; 271 C; 294 G; 432 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCGGACTGGCGATCGCATTTATTTCCTTCTCACGGATCGAT
                                                                                                                                           Claim 1; Fig 1; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                              21.8%;
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Best Local Similarity 55.7
Matches 754; Conservative
     1992-171652/21
                         P-PSDB; AAR24136.
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                CCTTCAAGTCAACCTCCGGCAGCATGACGACCTCTACAACATGATCAACACGTCAAAT
                                             2393 TTTTTAAAACTACTGATTCAAGTTCCAGTGAGTTGACTCAAATGATTTCAAGCGTTGCTT
                                                                            CCGACTGTCCAGACTCAACACTCCTGGGCACATTCGTCGAGAACCACGACCACGGT
                                                                                                          ccagricricgarccaacrricricacaacririgracaaarcacaraargaaaggr
                                                                                                                                                                                                      1075 ACGACGGAATCCCCATCATCTCTACGCCGGCCAAGAACAGCACTACGCCGGCGGAAACGACC
                                                                                                                                                                                                                                                                     CCGCGAACCGCGAAGCAACCTGGCTCTCGGGCTACCGGACCGACAGCGAGCTGTACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha amylase; carbohydrate hydrolase; increased activity;
tyrosine residue; enzyme centre; mass production; oligosaccharide;
variant; cyclomaltodextrin glucanotransferase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence TAY was mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variant alpha amylase deriv. from Saccharomyopsis fibuligera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1435 CGACCGTGACGGTTGGTTCGGATGGAAATGTGCCTGTTC 1473
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give a variant enzyme"
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247. .249
/*tag= a
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                                                                                                                       The plasmid may be used to transform an E.coli expression system for the stable production of amylase, useful in ethanol fermentation. See also AAN70917. (Updated on 24-OCT-2003 to standardise OS field)
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                                             Amylase prodn. - comprises culturing microorganism transformed with vector deoxyribonucleic acid, accumulating and collecting amylase.
                                                                                                                                                                                                                    Score 377.4; DB 1; Length 4214;
Pred. No. 9.1e-77;
0; Mismatches 626; Indels 15;
                                                                                                                                                                                       Sequence 4214 BP; 1249 A; 784 C; 860 G; 1321 T; 0 U; 0 Other;
                                                                                           Disclosure; Fig 1; 14pp; Japanese.
                                                                                                                                                                                                                   21.8%;
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Best Local Similarity 54.8
Matches 778; Conservative
WPI; 1987-173694/25
                P-PSDB; AAP70571
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Variant carbohydrate hydrolase(s) with increased activity - consists of e.g. alpha-amylase with tyrosine residue in enzyme centre, useful for mass-prodn. of oligosaccharide(s).
                                                                                                                                                                                                                                                                               Example 1; Page 13-15; 27pp; Japanese.
WPI; 1994-328987/41.
P-PSDB; AAR63184.
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AAQ77665-8 encode variant alpha amylases, composed by substituting bases 247-249 of the structural gene region, with TTC, TGG, CTC or AAC. These substitutions result in the 83rd amino acid residue (tyrosine) of the wild type sequence being changed to phenylalanine, tryptophan, leucine or asparagine respectively. The substituted amino acid is present in the active site of the enzyme and confers increased activity on the enzyme. The variants are useful for the mass production of oligosaccharides. (see AAQ77669 for the variant structure of a cyclomaltodextrin glucanotransferase)

Sequence 1404 BP; 406 A; 272 C; 293 G; 433 T; 0 U; 0 Other;

370 540 180 240 130 300 360 250 GGCAGCAGGATATATACTCTCTGAACGAAAACTACGGCACTGCAGATGACTTGAAGGCGC 420 GGATGAAGAACATATACAAAATTAATGAAACTTTGGTACTGCTGATGATTTGAAGTCTT 310 TCTCTTCGGCCCTTCATGAGAGGGGGATGTATCTTATGGTCGATGTGGGTTGCTAACCATA 480 430 AAGACTACTICCACCCGTICTGTTTCATTCAAAACTATGAAGATCAGACTCAGGTTGAGG 600 70 481 TGGGCTATGATGGAGCGGGTAGCTCAGTCGATTACAGTGTGTTTAAAACCGTTCAGTTCCC CTGCGGACTGGCGATCGCAATCCATTTATTTCCTTCTCACGGATCGATTTGCAAGGACGG crearaaareaacarcacacrerrrrarcaaarrercacreacacarrrecragaacce ATGGGTCGACGACTGCGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGAACATGGC AGGCCATCATCACCACCATGGACTATATCCAGGGAATGGGCTTCACAGCCATCTGGATCA CTCCAGTTGTTGAAAACATTCCCGATAACACACACATATGGTTATGCTTATCATGGTTTCT 371 ACGCCAGTGATGCCAGTGGAGATAGTATCGATTACTCAGAGTACACCCCGTTCAACGACC CCCCCGTTACAGCCCAGCTGCCCCAGACCACGCGTATATGGAGATGCCTACCATGGCTACT Score 375.4; DB 2; Length 1404; Pred. No. 2e-76; 0; Mismatches 586; Indels 15; 21.6%; Local Similarity 55.6 Query Match Best Local Si Matches 752 311 11 181 71 241 131 191 361 251 421 541 301 ઠ ద Š a 8 8 ò 8 6 8 6 6 6 8 S g

1020 1080 1140 1030 1090 ACCGCGAAGCAACCTGGCTCTCGGGCTACCCGACCGACGGGGCTGTACAAGTTAATTG 1200 CCTCCGCGAACGCAATCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA 1260 CGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCCTCTCCT 1380 irrccaacacacaciriacacriccercaegarrirecraeaacirrricacarecrecre 1315 850 900 790 960 970 caargaccagocaaagrrigarrrcraargcrarrocarriccarring Acadadadecerrerecerriarecederacaadadadadecerarracaadereare CCAAAGCTAATGCTGCCAGAAACGCCGCCGTTTATCAAGACTCAAGCTATGCCACCTCGC GTTCGGATCCAACTTTGTTGACAACTTTGTAGAAAATCACGATAATGAAAGGTTCGCTT GAATCCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGCGGAAACGACCCCGCGA GTATTCCTGTCATTACTATGGACAAGAACAAGGCTTGAGCGGAAAAAGTGACCCAAACA AGAACTGGCCCATCTACAAAGACGACACAACGATCGCCATGCGCAAGGGCACAGATGGGT AGAACGTCATGGACGGCGTACTGTCCCATTTACTATCCACTCCTCAACGCCTTCA AAACTACTGATTCAAGTTCCAGTGAGTTGACTCAAATGATTTCAAGCGTTGCTTCCAGTT GTCCAGACTCAACACTCCTGGGCACATTCGTCGAGAACCACGACAACCCACGGTTCGCTT CTTACACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACG ------reprincaacaaccrissiticascers TGAGTGGTGCGGGTTACACAGCCGGCCAGCAATTGACGGAGGTCATTGGCTGCACGG AGTCAACCTCCGGCAGCATGGACGACCTCTACAACATGATCAACACGGTCAAATCCGACT TGACGGTTGGTTCGGATGGAAATGTGCCTGTTC 1473 rraccecaecrereacrracaaerrreraree 1348 731 1031 1261 1151 1321 1381 1256 901 791 851 1021 911 971 1141 1201 1091 961 1001 셤 ò В 셤 Ś g ò 셤 8 B 8 셤 ò ద ર્જ 임 8 à

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611 TAAGAATTGATAGTGCTAAACATGTGGACCAAGGCTTTTTCCCGGATTTTGTTAGTGCAT

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Derived from plasmid pSf'1 (Agric. Biol. Chem.
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SEQUENCE CHRRACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNI
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PAPLICANT: MARGHI, IKUO

PAPLICANT: MARGHI, IKUO

PAPLICANT: MARGHI, IKUO

PAPLICANT: MAYAITI, Sachio

PAPLICANT: MAYAITION: Variant-Type Carbohydrate Hydrolase,

TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,

STREE: Birch, Stewart, Kolasch & Birch, LLP

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STREE: Birch, Stewart, Kolasch & Birch, LLP

COMPUTER: LBM P. Compatible

OMPUTER: Patchtln Release #1.0, Version #1.30

CUMPUTER: Patchtln Release #1.0, Version #1.30

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NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
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GTATTCCTGTCATTTACTATGGACAAGAACTAGGCCTTGAGCGGAAAAAGTGACCCAAACA 1030
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                                                                                                                                                                                                                                                                        CCTCCCCCAAACGCAATCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA 1260
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911 CAATGACCAGCGACCAAAGTTTGATTTCTAATGCTATTGCATTTGTCCTTTTGGGTGATG 970
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                                                        GAATCCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGCGGAAACGACCCCGCGA
                                                                                                                                                                APPLICANT: MATSUI, IKUO
APPLICANT: ISHTKAWA, KAZUHIKO
APPLICANT: ISHTKAWA, KAZUHIKO
APPLICANT: ISHTKAWA, KAZUHIKO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR ITILE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE: BIRCH STEWART, KOLASCH & BIRCH
STREET: 8110 Gatchouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: TC-LUCS/MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
PILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/204,656
FILING APPLICATION NUMBER: US/08/204,656
FILING APPLICATION NUMBER: 32,181
ATTONNEY/AGENT INPORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 33,181
REFERENCE/OCKET NUMBER: 33,181
TELEPAK: (703) 205-8000
TELEFAK: (703) 205-8000
TELEFAK: (703) 205-8000
TELEFEX: (703) 205-8050
TELEFEX: 248345
INFORMATION: FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
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STATE: Virginia
COUNTRY: U.S.A.
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| AAAAGTACTTCCATAACTACTGTCTTATTTCAAACTATGATGACGAGGTCAGGTTCAAA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 ATTGCTGGCTAGGAGATAACACTGTCTCCTTGCCTGATCTCGATACCACCAAGGATGTGG 660
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                                                                                                                                                                                      21.6%; Score 375.4; DB 1; Length 1404; 55.6%; Pred. No. 2.9e-98; ive 0; Mismatches 586; Indels 15;
                                                     /note= "Nucleotides 1-1404
correspond to nucleotides 79-1482 of
fibuligera '-amylase structural gene"
                                                                                                                                                                                                                                            752; Conservative
                         LOCATION: 1..1404
JOTHER INFORMATION:
OTHER INFORMATION:
CHER INFORMATION:
US-08-204-6568-7
                                                                                                                                                                                                                     Best Local Similarity
  NAME/KEY:
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1321 CGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCCTCTCCT 1380
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                                                                                                                              971 GTATTCCTGTCATTTACTATGGACAAGAACAAGGCTTGAGCGGAAAAAGTGACCCAAACA 1030
                                                                                                                                                                                                                                                        CCTCCGCGAACGCAATCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA 1260
                                                                                                                                                                                                                                                                                                  CCAAAGCTÀATGCTGCCAGAAACGCCGCCGTTTATCAAGACTCAAGCTATGCCACCTCGC 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCCAACACAGGTTACAGTTCCGGTGAGGATTTGGTAGAAGTTTTGACATGCAGTACTG 1315
                                           911 caargaccagcgaccaaagrrrgarrrcraargcrarrgcarrrcrcrrrrggrg 970
    CTTACACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACG
                                                                                       GAATCCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGCGGAAACGACCCCGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4. Application US/08467831
| Patent No. 5635378
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: ISHIKAWA, KAZUHIKO
| APPLICANT: MIYAIRI, SACHIO
| APPLICANT: MIYAIRI, SACHIO
| APPLICANT: MIYAIRI, SACHIO
| TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME | NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS: 17
| CORRESPONDENCE ADDRESS: 17
| ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH | STERET: BILO Gatchouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/08/467,831
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1441 TGACGGTTGGTTCGGATGGAAATGTGCCTGTTC 1473
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTOMNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22042
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                           Length 1404;
                                                                                                                                                                                         Score 375.4; DB 1; Length 1
Pred. No. 2.9e-98;
0; Mismatches 586; Indels
                                                                              MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
JS ANTI-SENSE: NO
US-08-470-702-4
                                                                                                                                                                                         Query Match
Best Local Similarity 55.6%;
Matches 752; Conservative
LENGTH: 1404 base pairs
                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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FOR PRODUCING

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CTTACACCAACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACG 1080
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                                                                                                                                                                                                                                                                                       1031 ACAGAGAGCCTTGTGGTTATCCGGCTACAAAGAGAGTGACTATTACAAGCTCATTG 1090
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APPLICANT: Mateau, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                         GAATCCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGCGGAAACGACCCCGCGA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
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Patent No. 5538882
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEFX: 248345
INFORMATION FOR SEQ ID NO: 1:
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NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,1
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STATE: Virginia
COUNTRY: U.S.A.
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STREET: 811
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                     Score 375.4; DB 1; Length 1404;
Pred. No. 2.9e-98;
0; Mismatches 586; Indels 15;
                                                                                                                                                           MOLECULE TYPE: DNA (synthetic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                  21.6%;
                          SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                            Best Local Similarity 55.6
Matches 752; Conservative
       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             , ANTI-SENSE: NO
US-08-467-831-4
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APPLICANT: Mateui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    CTTACACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCATCAACGACG
                                       AGTCAACCTCCGGCAGCATGGACGACCTCTACAACATGATCAACACCGTCAAATCCGACT
                                                                                                                       GTCCAGACTCCACCTCCTGGGCACATTCGTCGAGAACCACGACAACCCACGGTTCGCTT
                                                                                                                                                        851 GTTCGGATCCAACTTGTAGAAACTTTGTAGAAAATCACGATAATGAAAGGTTCGCTT
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                                                                               791 AAACTACTGATTCAAGTTCCAGTGAGTTGACTCAAATGATTTCAAGCGTTGCTTCCAGTT
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APPLICATION NUMBER: US/08/204,656B FILING DATE: O2-MAR-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                  CLONE: Derived from plasmid pSf'1 (Agric. Biol. Chem
                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
      LENUTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 751; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..1404
OTHER INFORMATION:
OTHER INFORMATION:
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APPLICANT: Mateui, Ikuo
APPLICANT: Ichikawa, Kazuhiko
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Bnzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
TAAGAATTGATAGTGCTAAACATGTGGACCAAGGCTTTTTCCCGGATTTTGTTAGTGCAT 670
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                                      CAGGCGTGTACTGTATCGGCGAGGTGCTCGACGGTGATCCGGCCTACACTTGTCCCTACC
                                                                              cregaerrracreagraegecaaerrrrecaaggagacceaecrraracarecearace
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                                                                                                                      AGAACGTCATGGACGCGTACTGAACTATCCCATTTACTATCCACTCCTCAACGCCTTCA
                                                                                                                                                                                                      AGTCAACCTCCGGCAGCATGGACGACCTCTACAACATGATCAACACCGTCAAATCCGACT
                                                                                                                                                                                                                                          791 AAACTACTGATTCAAGTTCAGTGAGTTGACTCAATGATTTCAAGCGTTGCTTCCAGTT
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Patent No. 5538882
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MEDIUM TYPE: Floppy disk
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STATE: Virginia
COUNTRY: U.S.A.
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correspond to nucleotides 79-1482 in the Saccharomycopsis
fibuligera '-amylase structural gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.6%; Score 373.8; DB 1; Length 1404;
55.5%; Pred. No. 8.3e-98;
iive 0; Mismatches 587; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                     Chem
                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE: CLONE: Derived from plasmid pSf'1 (Agric. Biol.
                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic nucleic acid"
            REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECHOWNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 751, Conservative
  Weiner, Marc S.
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1.1404
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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Patent No. 5631149
GENERAL INFORMATION
APPLICANT: MATSUI, IKUO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MUSENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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  GTTGCTGGGAAGGTGACTCTTCAGTTGCATTACCAGATTTGAGAACGGAAGATAGCGACG
                                         TCAAGAATGAATGGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATTGACGGCC
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correspond to nucleotides 79-1482 of
fibuligera '-amylase structural gene"
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Pred. No. 8.3e-98;
0; Mismatches 587; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: Derived from plasmid pSf'1 (Agric, Biol, Chem.
                  OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: other nucleic, acid
DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                    ATCORNEY AGENT INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEX: 248345
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       TELERAX: ...
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TVPE: nucleic acid
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al Similarity 55.5%;
751; Conservative
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OTHER INFORMATION:
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LOCATION: 1...
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Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI IKUO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HOWDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
601 ATTGCTGGCTAGGAGATAACACTGTCTCCTTGCCTGATCTCGATACCACGAAGGATGTGG
                                                                                                                       TCAAGAATGAATGGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATTGACGGCC
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                                                                                                                                                                                                                                                                                                          Version #1.25
:: BIRCH, STEWART, KOLASCH & BIRCH
8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MRR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WENNER, WARC S.
REGISTRATION NUMBER: 32,181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 33,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEFAX: (703) 205-8050
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HYPOTHETICAL: NO
ANTI-EPROT
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TELEX: 248345
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                    COUNTRY: U.S.A.
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US-08-470-702-1
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Best Local S:
Matches 751
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  431 AAAAGTACTTCCATAACTACTGTCTTATTTCAAACTATGATGACCAAGCTCAGGTTCAAA 490
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Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE (
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Pred. No. 8.3e-98;
0; Mismatches 587; Indels
                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: US/08/470,702
FILING DATE: 06-UNN-1995
                                         ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                 FILING DATE: vo-co...
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: OZ-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, WARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 334-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELERX: 248145
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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21.6%;
Best Local Similarity 55.5%;
Matches 751; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
                       CORRESPONDENCE ADDRESS:
JUMBER OF SEQUENCES:
                                                                                                               Virginia
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HYPOTHETICAL: N
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COUNTRY:
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                         CTGGAGTTTACTCAGTAGGCGAAGTTTTCCAAGGAGACCCAGCTTATACATGCCCATACC
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Patent No. 5635378
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
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VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING OLIGOSACCHARIDE USING THE ENZYME
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Pred. No. 8.3e-98;
0; Mismatches 587; Indels 15;
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION DATA:
FILING DATE:
APPLICATION NUMBER:
CLASSIFICATION A35
PROGRAPHON DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
TILING DATE:
APPLICATION NUMBER:
TILING DATE:
NAME:
NAME:
REGISTRATION NUMBER:
TRECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                    ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 55.5:
Matches 751; Conservative
  TITLE OF INVENTION: VA.
TITLE OF INVENTION: OL.
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                        COUNTRY:
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                   371 ACGGCAGTGATGGCAGTGGAGATAGTATCGATTACTCAGAGTACACCCCGTTCAACGACC
                                                            AAGACTACTTCCACCCGTTCTGTTTCATTCAAAACTATGAAGATCAGACTCAGGTTGAGG
                                                                                             431 AAAAGTACTTCCATAACTACTGTCTTATTTCAAACTATGATGACCAAGCTCAGGTTCAAA
                                                                                                                                            601 ATTGCTGGCTAGGAGATAACACTGTCTTGCCTGATCTCGATACCACCAAGGATGTGG
                                                                                                                                                                                   491 GTTGCTGGGAAGGTGACTCTTCAGTTGCATTACCAGATTTGAGAACGGAAGATAGCGACG
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; Sequence 2, Application US/08467831
; Patent No. 5635378
; GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
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                                    VARIANT-TYPE CARBOHYDRATE HYDROLASE,
VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
OLIGOSACCHARIDE USING THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATGAAGAACATATACAAAATTAATGAAAACTTTGGTACTGCTGATGATTTGAAGTCTT
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Pred. No. 8.3e-98;
0; Mismatches 587; Indels
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTONNEY/AGENT INFORMATION:
NAME: WERINER, MARC S.
REGISTRATION NUMBER: 32,181
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE H
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME,
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENTYMERS.
TUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Palls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32,181
RELECOMMUNICATION INFORMATION:
TELEPAN: (703) 205-8050
TELEFAX: 248745
                                                                                                                                                                                                                                          ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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E: DNA (synthetic)
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55.5%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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Best Local Similarity 55.5
Matches 751; Conservative
                                                                                                                                                                                                                             COUNTRY: U.S.A.
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STRANDEDNESS:
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                                           371 ACGGCAGTGATGGCAGTGGAGATAGTATTACTTCAGAGTACACCCCGTTCAACGACC
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US-08-467-831-3
; Sequence 3, Application US/08467831
; Patent No. 5635378
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APPLICANT: HONDA, KOICHI

TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,

TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING

TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME

TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME

CORRESPONDENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 8110 Gatchouse Road, Suite 500 East

CITY: Falls Church

STAFF: Virginia

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
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Pred. No. 8.3e-98;
0; Mismatches 587; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Ver SCHWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-UUN-1995
CLASSIFICATION A78:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
RECISTRATION NUMBER: 32,181
RECISTRATION NUMBER: 32,181
RECISTRATION NUMBER: 32,181
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  ISHIKAWA, KAZUHIKO
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MIYAIRI, SACHIO
HONDA, KOICHI
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.5
Matches 751; Conservative
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                             APPLICANT: MATSUI, II
APPLICANT: BISHKAWA,
APPLICANT: MIYAIRI, S
APPLICANT: HONDA, KO:
TITLE OF INVENTION: T
TITLE OF INVENTION: T
                                                                                                                                                                                                                                                                                                                                                                         CITY: Falls Church
STATE: Virginia
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   GENERAL INFORMATION:
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US-08-467-831-3
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ORGANISM: Artificial Sequence
SEATURE:
OTHER INFORMATION: DPR70 plasmid
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8.2%; Score 143; DB 4; Length 7432;
Best Local Similarity 54.1%; Pred. No. 2.1e-30;
Matches 513; Conservative 0; Mismatches 265; Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: RASMUSSEN, PREBEN
TITLE OF INVENTION: EXPRESSION ELEMENT
TITLE OF INVENTION: EXPRESSION ELEMENT
CURRENT APPLICATION NUMBER: US/09/367,891A
CURRENT APPLICATION NUMBER: US/09/367,891A
CURRENT APPLICATION NUMBER: PCT/1B98/00312
PRIOR PILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-367-891A-6/c
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54.1%; Pred. No. 1.3e-30;
tive 0; Mismatches 265; Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: amyA gene US-09-367-891A-5
Sequence 5, Application US/09367891A
Patent No. 6524816
GENERAL INFORMATION:
APPLICANT: RASMUSSEN, PREBEN
TITLE OF INVENTION: EXPRESSION ELEMENT
CURRENT APPLICATION UNMERE: US/09/367,891A
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: PCT/1B98/00312
PRIOR APPLICATION NUMBER: PCT/1B98/00312
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               848 CATGGACGCGTACTGAACTATCC-
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Best Local Similarity 54.19
Matches 513; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Unknown Organism
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1300 TTCTGACGCATGAGAACAGCTACTATCCTGCGCTTGATGCATTCAAGTCTGTCGGCGGCA 4241
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                                                                                                                                                                                                        976 TCCTGGGCACATTCGTCGAGAACCACGACAACCCACGGTTCGCTTC------ 1021
                                                                                                                                                                                                                                             4180 TGCTCGGCAATTTCCTTGAGAATCACGACATTGCTCGCTTTGCTTCGTATGGACACTCT 4121
                                                                                                                                                                                                                                                                                                                        4120 TTTGAAGCCCTCATCGATTGGGGATGCTGACAGGACAACAACAACAGGTACACGGATGA 4061
                                                                                                                                                                                                                                                                                                                                                                          1034 CATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACGGAATCCCCATCAT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTACGCCGGCCAAGAACAGCACTACGCCGGCGAAACGACCCCCGCGAACCAAGCAAC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 CTGGCTCTCGGGCTACCCGACCGACAGCTGTACAAGTTAATTGCCTCCGCGAACGC 1213
1360 GCTGGATGGCGTTCTGAACTATCCGATGTGAGTGATTCCGAAAGTTCCATCGATCAGGCT 4301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3940 cricicricricaciacaaraccaacccaagcreraccagricarcaagaagaccaarga 3881
                                        ------CATTTACTATCCACTCCTCAACGCCTTCAAGTCAACCTCCGGCA 915
                                                                                                                        916 GCATGGACGACCTCTACAACATGATCAACACGGTCAAATCCGACTGTCCAGACTCAACAC 975
                                                                                                                                                                                                                                                                                          -----TTACACCAACGA
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41 GAAGGCATTTATGATGGTCGCTGGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGC 100
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RESULT 15
US-09-189-060B-63
i Sequence 63, Application US/09189060B
i Patent No. 6270968
i GENERAL INFORMATION:
i APPLICANT: Balboge, Henrik
i APPLICANT: Sandal, Thomas
i APPLICANT: Borge, Diderichsen
i TILLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
i TILLE REFERENCE: 4772.204-US
i CURRENT APPLICATION NUMBER: US/09/189,060B
i CURRENT FILING DATE: 1998-11-10
i PRIOR FILING DATE: 1997-05-12
i NUMBER OF SEQ ID NOS: 74
i SEQ ID NO 63
i LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GATCCCATTIATGATGGTCGCGTGGTGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGC
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4.0%; Score 68.6; DB 3; Length 93;
Best Local Similarity 94.7%; Pred. No. 6e-10;
Matches 71; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
// OTHER INFORMATION: Primer US-09-189-0608-63
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Search completed: February 12, 2005, 02:00:17 Job time : 331 secs

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Sequence Sequence

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Sequence 47, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 36156, A
Sequence 5061, Appl
Sequence 1871, Appl
Sequence 1871, Appl
Sequence 3791, Appl
Sequence 105984,
Sequence 105984,
Sequence 107, Appl
Sequence 107, Appl
Sequence 107, Appl
Sequence 107, Appl
Sequence 24284, A
Sequence 24284, A
Sequence 177, Appl
Sequence 177, Appl
Sequence 177, Appl
Sequence 177, Appl
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Sequence 177, Appl
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Sequence 3, Appli
Sequence 31407, A
Sequence 31408, A
Sequence 332, App
Sequence 340, App
Sequence 340, App
Sequence 340, App
Sequence 342, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10820200
| Publication No. US20040229764A1
| GENERAL INFORMATION:
| APPLICANT: Bisgard-Frantzen, Henrik
| APPLICANT: Bisgard-Frantzen, Henrik
| APPLICANT: Bisgard-Frantzen, Henrik
| APPLICANT: Svendsen, Sven
| TILE REFERENCE: SVendsen, Allan
| TILLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
| FILE REFERENCE: 8385.200-US
| CURRENT APPLICATION NUMBER: US/10/820,200
| CURRENT APPLICATION NUMBER: US/09/710,339
| PRIOR PILING DATE: 2000-11-09
| PRIOR APPLICATION NUMBER: US 60/165,786
| PRIOR PILING DATE: 1999-11-16
| SOFTWARE: PatentIn version 3.2
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 1
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16 US-10-128-587A-28
17 US-10-128-578B-28
18 US-10-653-047-3796
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14 US-10-213-990-47
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18 US-10-13-990-46
19 US-10-369-493-3156
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14 US-10-287-465A-1
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19 US-10-287-465A-1
19 US-10-363-345A-31408
14 US-10-184-634-332
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US-09-216-393-342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: (54)..(1547)
OTHER INFORMATION: mat_peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Aspergillus Oryzae
                                 605
1644
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2364
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   RESULT 1
US-10-820-200-1
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   3775, Ap
41, Appl
44, Appl
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3837, Ap
                                                                                                           February 11, 2005, 21:34:18; Search time 949 Seconds (without alignments) 10781.241 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prihted, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                             Sequence 5
Sequence 4
Sequence 2
Sequence 3
Sequence 4
Sequence 4
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-653-047-5355

US-10-228-063-46

US-10-815-495-17

US-10-653-047-3775

US-10-653-047-3775

US-10-213-990-44

US-10-653-047-38377

US-10-653-047-38377

US-10-653-047-38377

US-10-128-590-28
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                                                                                                                                                                                                                                                                                         5378673 segs, 2950229984 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length
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22443
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221.345.5344
21.345.534.534
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Gaps

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1011.2 979 908.2 806 786 648.2

Result Š 439 374.2 369.2

| 091 GANTCCCCATCATCTAGGCCGGCCAAGAACAGCACTACGCCGGGAAACGCCCCCGCA 1140 1091 GANTCCCCATCATCTAGGCCGGCCAACACTCCCCGGGGAAACGCCCCCCCC | RESULT 2 US-10-653-047-5355 i Sequence 5555, Application US/10653047 i Publication No. US20040229367A1 i GENERAL INFORMATION: APPLICANT: Michael W. Rey APPLICANT: Michael W. Rey APPLICANT: Michael W. Rey APPLICANT: Askari Kaupphnen APPLICANT: Deferey R.Shuster APPLICANT: Deferey R.Shuster APPLICANT: Bakari Kaupphnen APPLICANT: Bakari Kaupphnen APPLICANT: Borch Clausen APPLICANT: Borch Clausen APPLICANT: Borch Clausen APPLICANT: Borch Clausen APPLICANT: Borch Clausen APPLICANT: Borch Clausen APPLICANT: Borch Clausen APPLICANT: Borch Clausen APPLICANTION: Expression TITLE OF INVENTION: Expression TITLE OF INVENTION: WHRER: US/10/653,047 CURRENT FILING DATE: 2000-03-22 PRIOR FILING DATE: 2000-03-22 PRIOR FILING DATE: 1999-03-22 NUMBER OF SEQ ID NOS: 7860 SOFTWARE: FastEEQ for Windows Version 4.0 SEQ ID NO 5355 LENGTH: 1914 TYPE: DA TYPE: DA VEGANISM: Aspergillus oryzae US-10-653-047-5355 |
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| | 1141 ACGGGAAGCAACTTGGGGCTACCCGACGACAGCGACGCTGTACAAGTTAATTG | 1201 CCTCCGCGAACGCAATCCGGAACTATTAGCAAAGATACAGGATTCGTGAACTACA 1203 CCTCCGCGAACGCATCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA | 1261 AGAACTGGCCCATCTACAAAGACGACGACGCCATGCCCAGGGCGCACAGGTGGGT | 1321 CGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCTTCTCTCTTCTTTTTTTT | 1381 TGAGTGGGGGTTACAGGGCGGCGGCAGGAATTGAGGGAGG | 1441 TGACGGTTGGTTCGGATGGAAATGTCCCTGTTCCTATGGCAGGTGGGCTACGTAGGGTATGTTCTATGGCAGGTGGGCTACCTAGGGTATGTAGGTAG | 1501 TGTATCCCACTGAGAAGTTGGCAGGTAGCAGATCTGTAGTAGTGGTGGTGGAGATTGGTGGAGATTGGTGGAGATTGGTGG | 1561 GTATATGATGGTACTGCTATTCAATCTGGCATTGGACGTGAGTTTGAGTTTGATGTACA [| 1621 GTTGGAGTCGTTACTGCTGTGATCCCCT | Oy 1681 CCAAGCAGTTATTATAGGAAA 1707 | RESULT 3 US-10-228-063-46 ; Sequence 46, Application US/10228063 | ; FUDICATION NO. USZOJJISOBOSAL ; GENERAL INFORMATION: ; APPLICANT: Lanahan, Mike ; TITLE OF INVENTION: Self-processing Plants and Plant Parts | ; CURRENT ABLEICATION WHERE: US/10/228,063 ; CURRENT FILLICATION DATE: 2002-12-12 ; NUMBER OF SEQ ID NOS: 60 | ; SCOFTWARE: FASESEQ FOR WINDOWS VERBION 4.0 ; SEQ ID NO 46 ; LENGTH: 3285 ; TYPE: DNA ; OCCANITON: 6 pironesmi | 08 | H 5-5 |
|---|--|---|--|--|--|---|--|---|--|---|---|---|--|---|---|---|
| Query Match 98.4%; Score 1707; DB 18; Length 1914; ; Best Local Similarity 100.0%; Pred. No. 0, 0, 0 Gaps 0; Matches 1707; Conservative 0, Mismatches 0; Indels 0; Gaps 0; Qy 1 TCACATCAAGCTCTCCCTTCTGAACAACAAAACCCCACAGAAAGGCATTTATGATGGTGG 60 1 | dy 61 CGTGGTGGTCTCTATTTCTGTACGGCCTTCAGGTCGGGACCTGCTTTGGCTGCAACGC 120 Db 63 CGTGGTGGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCACGC 122 | Qy 121 CTGCGGACTGGCGATCGCATTTATTTCCTTCTCAGGATCGATTTGCAAGGACGG 180 D 123 CTGCGGACTGGCGATCGCATTTATTTCCTTCTCACGGATCGATTTGCAAGGACGG 182 | Qy 181 ATGGGTCGACGACTTGTAATACTGCGGATCAGAATACTGTGGTGGAACATGGC 240 | Qy 241 AGGGCATCATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGCCATCTGGATCA·300 | Qy 301 CCCCGTTACAGCCCAGCTGCCCCAGACCACCGCATATGGAGATGCCTACCATGGCTACT 360 | Qy 361 GGCAGCAGCAGATATATACTCTCTGAACGAAAACTACGGCACTGCAGATGACTTGAAGGCGC 420 | Qy 421 TCTCTTCGGCCCTTCATGAGAGGGGATGTATCTTATGGTCGATGTGGTTGCTAACCATA 480 | Qy 481 TGGGCTATGATGGAGGGGTAGCTCGATTACAGTGTTTAAACCGTTCAGTTCC 540 Db 483 TGGGCTATGATGGAGGGGTAGCTCAGTCGATTACAGTGTGTTTAAACCGTTCAGTTCC 542 | Qy 541 AAGACTACTTCCACCGTTCTGTTTCAAAACTATGAAGATCAGACTCAGGTTGAGG 600 | Qy 601 ATTGCTGGCTAGGAGATAACACTGTCTCCTTGCCTGATTCTCGATACCACCAAGGATGTGG 600 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Qy 661 TCAAGAATGAATGGTACGACTGGGATCATTGGTATCGAACTACTCCATTGACGGCC 720 Db 663 TCAAGAATGAATGGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATTGACGGCC 722 | OY 721 TCCGTATCGACACAGTAAAACGCCTCCAGAAGGACTTCTGGCCCGGGTACAAAGCCG 780 | OY 781 CAGGGGGTGTACTGTATCGGCGAGGTGCTCGACGGTGATCCGGCCTACACTTGTCCCTACC 840 | OY 841 AGAACGTCATGGACGGCGTACTGAACTATCCCATTTACTATCCACTCCTCAACGCCTTCA 900 | dy 901 AGTCAACCTCCGGCAGGATGGACGACCTCTACAACATGATCAACACGTCAAATCCGACT 960 bb 903 AGTCAACCTCCGGCAGCATGGACCACCTCTACAACATGATCAACACGTCAAATCCGACT 962 | GTCCAGACTCAACACTCCTGGGCACATTCGTCGAGAACCACGACAACCAGGGTTCGCTT |

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               1141 ACCTACAAGAACTGGCCGATCTACAAGGACGACGACCACCATCGCCATGCGCAAGGGCACC
                                                       GATGGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACC
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                                                                        Accaccergaccergeerrccaacecaacereccesreccearedccacecescercce
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                                                                                                                                                                                                                                                                                                                                ; Sequence 17, Application US/10815495; Publication No. US20040191864A1; GENERAL INFORMATION:
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ORGANISM: Aspergillus niger
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NAME/KEY: misc feature
LOCATION: (10) ...(10)
CTHER INFORMATION: n=a,c,g
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                                                                                                                              TGGATCACCCCGTTACAGCCCCAGCTCCCCAGACCACCGCATATGGAGATGCCTACCAT
                                                                                                                                              TGGATCACCCCGGTGACCGCCCAGCTCCCGCAGACCACCGCCTACGGCGACGCCTACCAC
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             AGGACGGATGGGTCGACGACTGCGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGA
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| 1022 | 1216 TCCGGAACTATGCCATTAGCAAGATACGGGATTCGTGACCTACA | 0y 1437 ACCGTGACGGTTGGATGGAAATGTGCCTGTTCCTATGGCAGGTGGCTACCTAGG 1496 Db 2131 ACCGTGACGGTTGGTTCGGATGGAAATGTGCCTGTTCCTATGGCAGGTGGCTACCTAGG 2190 Oy 1497 GTATTGTATCCGACTGAGAAGTTGGCAGTAGCTGTAGTAGCTCGTGAAGGGT 1556 Db 2191 GTATTGTATCCGACTGAGAAGTTGGCAAGATCTGTAGTAGTAGCTCGTGAAGGGTG 1556 Db 2191 GTATTGTATCCGACTGAGAAGTTGGCAAGATCTGTAGTTGATGTGTG 2250 Oy 1557 GAGAGTATATGATGGTATTCAATCTGGCATTGGACAGTGAGTTGATTGA | RESULT 5 US-10-815-495-21 Sequence 21, Application US/10815495 Sequence 21, Application US/10815495 Sequence 21, Application No. US20040191864A1 Sequence 21, Application No. US20040191864A1 GENERAL INFORMATION: APPLICANT: Worozymes Biotech, Inc. APPLICANT: Connelly, Mariah TITLE OF INVENTION: Mathods For Producing Biological Substances In Enzyme-Deficient TITLE OF INVENTION: Mathods For Producing Biological Substances In Enzyme-Deficient TITLE OF INVENTION: MATHORS OF ASPERSION SOFTILE REFERENCE: 10345.200-US CURRENT APPLICATION NUMBER: US/10/815,495 CURRENT APPLICATION NUMBER: US/10/815,495 CURRENT PREVENT FILING DATE: 2004-03-31 NUMBER OF SEQ ID NOS: 30 SOFTWARE: PatentIn version 3.2 SEQ ID NO 21 LENGTH: 2520 TYPE: DNA ORGANISM: Aspergillus niger FEATURE: FEATURE: |
| 0 0 0 0 1 0 | | 1 1 10 1 10 1 10 1 10 10 10 10 10 10 10 | 5 5 5 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |
| | CTACGGCACTGCAGATGACTTGAAGGGGCTCTTCGGCCCTTCATGAGGGGGGGATGTA 451 | 68 68 11 11 11 11 12 12 12 | |
| 256 - 281 7 281 7 511 7 511 7 511 7 511 7 611 7 611 7 691 7 | 392 CTACGGCA 751 CTACGGCA 452 TCTTATGG 811 TCTTATGG 482 871 GATATGGT 504 TCACTCGA 504 TCACTCGA 504 TCACTCGA 564 TTCATTCA | | 806 GCTCGACGGT 1291 GCTCGACGGT 866 CTATCCCATC 1351 CTATCCCATG 875 1411 ACGGCTAAAA 921 GACGACCTCT 921 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACCTCT 1471 GACGACTTCG 1531 GGCACATTCG |

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                                                                               541 GACGGTTGGTTCGGATGGAAATGTGCCTGTTCCTATGGCAGGTGGGCTACCTAGGGTATT
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Sequence 41, Application US/10213990

Sequence 41, Application US/10213990

BUBLICANT: US-08000082595A1

APPLICANT: Jiang, Bo

APPLICANT: Storms, Howard

APPLICANT: Roemer, Terry

TITLE OF INVENTION: BNICEEC ACIDS OF ASPERGILLUS FUMI

TITLE OF INVENTION: BNICEEC ACIDS OF USE

TITLE OF INVENTION: BNICEEC ACIDS OF USE

TITLE OF SINGENION NUMBER: US/10/213,990

CURRENT APPLICATION NUMBER: US/10/213,990

CURRENT APPLICATION NUMBER: US/10/213,990

SOFTWARE: FREESE OF ID NOS: 72

SOFTWARE: FREESE OF IN MOS: 72

SOFTWARE: FREESE OF IN MOS: 73

SOFTWARE: RASEG FOR WINDOWS VERSION 4.0

SEQ ID NO 41

LENGTH: 1488

TYPE: DNA

ORGANISM: Aspergillus
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                                                                                                                                                                                                                                                                                                                                                                            CAAGCACGCTAGTCTATTATAGGAAA 1707
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Sakari Kauppinen
APPLICANT: Sakari Kauppinen
APPLICANT: Defer Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring, Multiple Gene
TITLE OF INVENTION: Methods For Monitoring, Multiple Gene
TITLE OF INVENTION: Mothers: US/10/653,047
CURRENT APPLICATION NUMBER: US/09/533,559
FRIOR APPLICATION NUMBER: US/09/533,559
PRIOR APPLICATION NUMBER: US/09/533,562
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3775
LENGTH: 1389
                                                                               2191 GTATTGTATCCGACTGAGAAGTTGGCAGGTAGCAAGATCTGTTACGGCT
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Pred. No. 8.1e-239;
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al Similarity 100.0%; Pred. No. 8.1
806; Conservative 0; Mismatches
                                                                                                                                                                                   Sequence 3775, Application US/10653047
Publication No. US20040229367A1
GENERAL INFORMATION:
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US-10-653-047-3775
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18-10-213-990-44
Sequence 44, Application US/10213990
Publication No. US20030082595A1
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
         1418 CCATGGCTAGTGGCTTGCCCCGGGTGTTTTACCCAACGGCTGGACGAACGGAAGTACTG 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/213,990 CURRENT FILING DATE: 2002-08-05 NUMBER OF SEQ ID NOS: 72 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 44 LENGTH: 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.4
Matches 966; Conservative
                                                         1534 TCTGTAGTAG 1543
                                                                                                 1478 TTTGTACTTG 1487
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; LOCATION: (1)...(1893)
US-10-213-990-44
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ORGANISM: Aspergillus
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                 TILLE OF INVENTION: Methods For Monitoring Multiple Gene; TILLE OF INVENTION: Methods For Monitoring Multiple Gene; TILLE OF INVENTION: Expression; FILE REFERENCE: 5849.2004.02
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR PLILIAGION NUMBER: 09/273,623
; PRIOR FILING DATE: 2000-03-22
; PRIOR FILING DATE: 1999-03-22
; RICH FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SCOTWARE: FaatsEQ for Windows Version 4.0
; SEQ ID NO 3775
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Best Local Similarity 98.9%;
Matches 442; Conservative
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; ORGANISM: Aspergillus niger
US-10-653-047-3775
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GGTATGATTGGGTGAAGGGATTGGTTGCCAACTACTCCCATCGACGGCCTGCGCATCGACA
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                                                                  GGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATTGACGGCCTCCGTATCGACA
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US-10-653-047-3775/C
Sequence 3775, Application US/10653047
Publication No. US20040229367A1
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Offirey R. Shuster
APPLICANT: Sakari Kauppinen
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Score 439, DB 18, Length 1389, Pred. No. 7e-125, 0, Mismatches 5, Indels 0

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Sequence 3837, Application US/10653047

Publication No. US20040229367A1

GENERAL INFORMATION:

APPLICANT: Randy M. Berka

APPLICANT: Adfrey S. Shuster

APPLICANT: Sakari Kauppinen

APPLICANT: Beter Bjarke Olsen

APPLICANT: Beter Bjarke Olsen

TILLE OF INVENTION: Methods For Monitoring Multiple Gene

TILLE OF INVENTION: Expression

TILLE OF INVENTION: Methods For Monitoring Multiple Gene

TILLE OF INVENTION: Expression

TILLE OF INVENTION: Methods For Monitoring Multiple Gene

TILLE OF INVENTION: Methods For Monitoring Multiple Gene

TILLE OF INVENTION: Expression

FILLE REPRENCE: 5849, 200-US

CURRENT PLILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US/10/533,047
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                                                                                                                                                               Query Match 21.6%; Score 374.2; DB 18; Length 483; Best Local Similarity 91.0%; Pred. No. 5.1e-105; Matches 443; Conservative 0; Mismatches 35; Indels 9;
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Publication No. US20030108561A1
GENERAL INFORMATION:
TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
FILE REFRENCE: 135 PCT
CURRENT APPLICATION WUMBER: US/10/128,590
CURRENT APPLING DATE: 2002-07-22
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 4190
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3837
LENGTH: 483
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                                                                         i TYPE: DNA
i ORGANIUSM: Aspergillus niger
i FEATURE:
i NAME/KEY: misc_feature
i LOCATION: (1)...(483)
OTHER INFORMATION: n = A,T,C or
US-10-653-047-3837
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; ORGANISM: vector pMF30
US-10-128-590-28
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US-10-128-590-28/c
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   Length
Query Match 21.3%; Score 369.2; DB 15; Length Best Local Similarity 54.6%; Pred. No. 6e-103; Matches 759; Conservative 0; Mismatches 628; Indels
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Publication No. US20030152940A1

GENERAL INFORMATION:

TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
TITLE OF INVENTION: Directins
TITLE OF INVENTION: Directins
TITLE OF INVENTION: Directins
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Publication No. US20040229367A1
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Andrhael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jeffrey R.Shuster
APPLICANT: Ib Groth Clausen
APPLICANT: Ib Groth Clausen
APPLICANT: Ib Groth Clausen
APPLICANT: Meter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1611 ATGGCTCGACCACAGCTGATTAGTGAGTGATCGCAAGTACTGTGGGGATCTTATA 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1551 AAGGGATTATCGACAAGTTGGATTATATTCAAGGTATGGGTTTCACTGCGATCTGGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Vector pMF30; OTHER INFORMATION: sequence
US-10-128-578B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
21.3%; Score 369.2; DB 17; Length 4190;
Best Local Similarity 54.6%; Pred. No. 6e-103;
Matches 759; Conservative 0; Mismatches 628; Indels 3;
                                                                                                                                                                                                                                Sequence 28, Application US/10128578B
; Bublication No. US20030211597A1
; GENERAL INFORMATION:
; APPLICANT: BOSMAN, FONS
; APPLICANT: DESCHAMFS, GERT
; APPLICANT: SARLON, ERWIN
; APPLICANT: SARLON, ERWIN
; APPLICANT: SARLON, ERWIN
; APPLICANT: SARLON, ERWIN
; APPLICANT: HALEWYN, JOOST
; TITLE OF INVENTION: EXPRESSION OF CORE-GLYCOSYLATED HCV ENVE
; TITLE OF INVENTION: EXPRESSION OF CORE-GLYCOSYLATED HCV ENVE
; FILE REFERENCE: 2551-73
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PARENTIN VERSION 2.1
; SEQ ID NOS: 65
; SOFTWARE: PARENTIN VERSION 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
       1501 TGTATCCGAC 1510
                                                                          ACCUTCCTC 285
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GCAACCTGGCTCTCGGGCTACCCGACCGACAGCGAGCTGTACAAGTTAATTGCCTCCGCG 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 GCATTCTACACTGACAGCACACCATCGCAATGCGCAAAGGCACCTCAGGGAGCCAAGTC
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                                                                                                                                                                                                                                                                                                                                    Query Match
19.9%; Score 344.2; DB 18; Length
Best Local Similarity 67.7%; Pred. No. 1.6e-95;
Matches 481; Conservative 0; Mismatches 229; Indels
  PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 2000-03-22
PRIOR PELING DATE: 2000-03-22
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SEQ ID NO 3776
LENGTH: 1048
TYPE: DA
TYPE: DA
TYPE: DA
TYPE: OA
TYPE: Mac feature
CRGANISM: misc_feature
LOCATION: (1)...(1048)
OTHER INFORMATION: n = A,T,C or G
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Pred. No. 2.7e-103;
0; Mismatches 7; Indels 5;
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Publication No. US20040229367A1
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Randy M. Berka
APPLICANT: Sakari Kauppinen
APPLICANT: Sakari Kauppinen
APPLICANT: Sakari Kauppinen
APPLICANT: Peter Bjarke Olean
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: S849.200-US
CURRENT APPLICATION NUMBER: US/10/653,047
FILE OF INVENTION: Expression
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT APPLICATION NUMBER: US/09/533,559
FRIOR APPLICATION NUMBER: US/09/533,559
FRIOR FILING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: 09/273,623
FRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FRSELSEQ FOR Windows Version 4.0
SEQ ID NO 3796
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21.3%;
Best Local Similarity 97.2%;
Matches 418; Conservative
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LOCATION: (1)...(605)
COLER INFORMATION: n = A,T,C US-10-653-047-3796
                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Aspergillus niger
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US-10-653-047-3776
                                                                                                                                                                                                                              LENGTH: 605
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February 11, 2005, 19:15:18; Search time 6083 Seconds (without alignments) 11636.883 Million cell updates/sec
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    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                          OM nucleic - nucleic search, using sw model
                                                                                      IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                             US-10-820-200-1
1734
                                                                    Perfect score:
                                                                                      Scoring table:
                                                                          Sequence:
                                                                                                       Searched:
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Sequence 7, Appli
Sequence 7, Appli
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24 US-09-533-559-5355

58 US-10-653-047-5355

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GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Broaden, Sven
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
FILE REPERENCE: 5835, 200-US
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/165,786
NUMBER OF FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 1 0; Indels 100.0%; Score 1734; DB 32; 100.0%; Pred. No. 7.8e-252; iive 0; Mismatches 0; FEATURE:
NAME/KEY: CDS
LOCATION: (54)..(1547)
CTHER INFORMATION: mat_peptide
US-09-710-339-1 TYPE: DNA ORGANISM: Aspergillus Oryzae Best Local Similaricy .vv. Matches 1734; Conservative LENGTH: 1734 US-09-710-339-1 н 121 181 181 241 241 301 361 541 541 601 61 61 121 301 361 421 421 481 481 601 Query Match 셤 g 셤 ઠે g 셤 ò 셤 à 셤 ò 셤 ò 셤 ò ò ò ò ò ઠે

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241 AGGGCATCATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGCCATCTGGATCA
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                         Sequence 1, Application US/09710339A
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bedersen, Sven
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamy1-like Alpha-Amylase Variants
FILE REFERENCE: 5355, 200-02
CURRENT APPLICATION NUMBER: US/09/710,339A
CURRENT APPLICATION NUMBER: US 60/165,786
PRIOR APPLICATION NUMBER: US 60/165,786
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1734
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FEATURE:
NAME/KEY: CDS
LOCATION: (54)..(1547)
COTHER INFORMATION: mat_peptide
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (114)..()
COTHER INFORMATION:
US-09-710-339A-1
100.0%;
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ORGANISM: Aspergillus Oryzae
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APPLICANT: Bedersen, Sven
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
FILE REFERENCE: 5835.200-US
CURRENT FILING DATE: 2000-11-09
FRIOR PILING DATE: 2000-11-09
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
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                                                                                               ; Sequence 1, Application US/09710339B
; GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (54)..(1547)
OTHER INFORMATION: mat_peptide
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (114)..(1733)
US-09-710-339B-1
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| | RESULT 4 US-10-820-200-1 ; Sequence 1, Application US/10820200 ; GENERAL INFORMATION: ; APPLICANT: Bisgard-Frantzen, Henrik | ; APPLICANT: Pedersen, Sven ; APPLICANT: Svendsen, Allan ; ITILE OF INVENTION: FUNGAMY1-like Alpha-Amylase Variants ; FILE REFERENCE: 5835.200-US ; CURRENT APPLICATION NUMBER: US/10/820,200 ; CURRENT FILING DATE: 2004-04-07 | ; PRIOR APPLICATION NUMBER: US/09/710,339 ; PRIOR FILING DATE: 2000-11-09 ; PRIOR APPLICATION NUMBER: US 60/165,786 ; PRIOR FILING DATE: 1999-11-16 | ; NUMBER OF SEQ ID NOS: 5 ; SOTWARE: Patentin version 3.2 ; SEQ ID NO 1 ; LENGTH: 1734 | TYPE: DNA CONTROL OF STATE CONTROL OF ST | COCATION: (54)(1547) COTHER INFORMATION: mat_peptide FEATURE: NAME/KEY: mat_peptide | 733) 100.0%; Score 1734; DB | Pred. 0; Miss CTCTGAA | 1 TCACATCAAGCTCTCCCTTCTGAACAATAAACCCCACAGAAGGCATTTATGATGGTCG 61 CGTGGTGGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGCACCTTGGTTTAGGTCG | | Db 121 CTGCGGACTGCGATCCATTATTACTTCACGGATCGATTGCAAGGACGG 180 Qy 181 ATGGGTCGACTGCAACTTGTAATACTGCGAAAATACTGGGGACGG 240 | Db 181 ATGGGTCGACGACTTGTAATACTGCGGATCAGAAATACTGTGGTGGAACATGGC 240 Qy 241 AGGCATCACGAAGATGGACTATATCCAGGGAATGGGCTTCACAGCCATCTGGATCA 300 | 241 | OY 301 CCCCGTTACAGCCCCCAGAACCACACACACACACACACAC | | 421 TCTCTTCGGCCCTTCATGAGGGGGATGTATCTTATGGTCGATGTGGTTGCTAACCATA |
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| | Qy 661 TCAAGAATGATACGACTAGGATCATTGGTATCGAACTACCAATTGACGGC 720 D | | dy 841 AGAACGTCATGGACGGGTACTGAACCATTTACTATCCACTCCTCAAGGCCTTCA 900 Db 841 AGAACGTCATGGACGGCGTACTGAACTATCCCATTTACTATCCACTCCTCAAGGCCTTCA 900 | OY 901 AGTCAACCTCCGGCAGCATGGACGACCTCTACAACATGATCAACACGTCAAATCCGACT 960 | QY 961 GTCCAGACTCAACACTCCTGGGCACATTGGTCGAGACACCAGGCACGCTTGGCTT 1020 L | OY 1021 CTTACACCAACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACG 1080 | QY 1081 GAATCCCCATCATCTACGCCGGCCAAGAACAGCACGCGGGGAAACGACCGCGGG 1140 Db 1081 GAATCCCCATCATCTACGCCGGCCAAGAACAGCACTACGCCGGGGGAAACGACCCCGCGG 1140 | Qy 1141 ACCGCGAACCTGGCTCTCGGGCTACCCGACCGCGAGCTGTACAAGTTAATTG 1200 Db 1141 ACCGCGAACCAACCTCGGGCTACCCGACCGAACGGAGCTGTACAAGTTAATTG 1200 | CCTCCGCGAACGCAATCCGGAACTATGCCATTAGCAAAGATACGGATTCGTGAC | 1261 AGAACTGGCCCATCTACAAAGACGACAACGATGCCATGCGCAAGGGCACAGATGGGT | Qy 1321 CGCAGATCGTGACTATCTTGTCCAACAGGTGCTTCGGGTGATTCGTATACCCTCTCCT 1321 CGCAGATCGTGACTATCTTGTCCAACAAGGTGCTTCGGGTGATTCGTATACCCTCTCCT 1321 CGCAGATCGTGACTATCTTGTCCAACAAGGTGCTTCGGGTGATTCGTATACCCTCTCCT 1380 | Oy 1381 TGAGTGGGGGTTACACAGCCGGCCAGCAATTGACGGAGGTCATTGGCTGCACGACG 1440 | GTAT | 1501 TGTATCCGACTGAGAAGTTGGCAGGTAGCAAGATCTGTAGTAGCTCGTGAGGGTAGCTGGCGTAGCAAGATCTGAGAGGGTAGCTGGCAGGTAGCTGGCAGGTAGTGGCAGGTAGTGGCAGGTAGTGGCAGGTAGTGGCAGGTAGTGGTAGTGGTAGTGGTAGTGGTAGTGGTAGTGGTAGTGGTAGGTAGTGGTAGGGTAGG | GTATATGATGGTACTGCTATTCAATCTGGCATTGGACAGTGAGTTTGAGTTTGATGTACA | 1621 GTTGGAGTCGTTACTGCTGTCATCCCTTATACTCTTCGATTGTTTTTCGAACCCTAATG |

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JOURDAYT: Randy W. Berka
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R. Shuster
APPLICANT: Jeffrey R. Shuster
APPLICANT: Defrey R. Shuster
APPLICANT: Deter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
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TITLE OF INVENTION WUMBER: US/09/533,559
CURRENT APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FESTERE FILING DATE: 1999-03-22
ILBNGRARE: FESTERE FILING DATE: 1999-03-22
SOFTWARE: FESTERE FILING DATE: 1999-03-22
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Pred. No. 9.1e-248;
0; Mismatches 0;
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8.09-533-559-5355
9. Sequence 5355, Application US/09533559
GENERAL INFORMATION:
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Conservative 0;
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APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Geffrey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Deter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
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TITLE OF INVENTION: Mynder: US/10/653,047
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
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APPLICANT: Tragi, Shinobu
APPLICANT: Alain, Eric
APPLICANT: Hjort, Caraten
APPLICANT: Hjort, Caraten
APPLICANT: Vikso-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PRO
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PRO
CURRENT APPLICATION NUMBER: PCT/USO4/20499
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.3
SEQ ID NO 39
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FEATURE:
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                                                                                                   APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Traira, Rikako
APPLICANT: Traira, Rikako
APPLICANT: Aliain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Hjort, Carsten
APPLICANT: Vikso-Vialsen, Anders
APPLICANT: Vikso-Vialsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SSEQ ID NOS: 43
SSEQ ID NO 39
LENGTH: 1827
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86.4%; Score 1497.8; DB 64;
Best Local Similarity 99.9%; Pred. No. 3.2e-216;
Matches 1499; Conservative 0; Mismatches 2;
                                                                               ; Sequence 39, Application US/10877849
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Artificial
                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS
; LOCATION: (1)..(1827)
US-10-877-849-39
                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial
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APPLICANT: Tkagi, Shinobu
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Hjort, Carsten
APPLICANT: Vikso-Nielsen, Anders
TITLE OP INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
TITLE REPERENCE: 10490.500-US
CURRENT APPLICATION NUMBER: PCT/US04/20499
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SSOTWARE: Patentin version 3.3
SEQ ID NO 35
LENGTH: 1923
                                                                                                                                 TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INPORMATION: Artificial
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Matches 1498; Conservative
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; LOCATION: (1)...
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PCT-US04-20499-35
; Sequence 35, Application PC/TUS0420499
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako

ö 113 173 61 GCAACGCCTGCGGACTGGCGATCGCAATCCATTATTTCCTTCTCACGGATCGATTGCA 120 180 ACATGGCAGGCATCATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGCCATC 240 360 473 420 533 480 593 540 653 900 713 9 773 233 293 353 413 9 GGCTACTGGCAGCAGGATATATATACTCTCTGAACGAAAACTACGGCACTGCAGATGACTTG GGCTACTGGCAGGAGGATATATACTCTCTGAACGAAAACTACGGCACTGCAGATGACTTG AACCATATGGGCTATGATGGAGCGGGTAGCTCAGTCGATTACAGTGTGTTTAAACCGTTC AGTICCCAAGACTACTICCACCCGTICTGTITCATICAAAACTATGAAGAICAGACTCAG AGTICCCAAGACTACTICCACCCGTICTITITITITITITICAAAACTATGAAGATCAGACTCAG GTTGAGGATTGCTGGCTAGGAGATAACACTGTCTCCTTGCCTGATCTCGATACCACCAAG GTTGAGGATTGCTGGCTAGGAGATAACACTGTCTCCTTGCCTGATCTCGATACCACCAG GACGGCCTCCGTATCGACACAGTAAAACACGTCCAGAAGGACTTCTGGCCCGGGTACAAC GCAACGCCTGCGGACTGGCGATCGCATTTATTTCCTTCTCACGGATCGATTTGCA AAGGCGCTCTTCGGCCCTTCATGAGGGGGGATGTATCTTATGGTCGATGTTGCT AACCATATGGGCTATGATGAGGGGGGGGTAGCTCAGTCGATTACAGTGTGTTTAAAACCGTTC GATGTGGTCAAGAATGAATGGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATT GATGTGGTCAAGAATGAATGGTACGACTGGGTGGGATCATTGGTATCGAACTACTCCATT 121 AGGACGGATGGGTCGACGACTAGCAATACTGCGGATCAGAAATACTGTGGTGGA TGGATCACCCCCGTTACAGCCCAGCTGCCCCAGACCACCGCATATGGAGATGCCTACCAT 54 ATGGTCGCGTGGTGGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCT 1 ATGGTCGCGTGGTGTCTCTATTTCTGTACGGCCTTCAGGTCGCGGCACCTCTGCTTTGGCT AGGACGGATGGGTCGACGACTTGTAATACTGCGGATCAGAAATACTGGTGGA Gaps 86.4%; Score 1497.4; DB 2; Length 1923; 99.9%; Pred. No. 3.6e-216; ive 0; Mismatches 1; Indels 0; 601 714 661 g δ 셤

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                                                                                                            Score 1497.4; DB 64
Pred. No. 3.6e-216;
0; Mismatches 1;
   FEATURE: OTHER INFORMATION: Artificial
                                                                                                            Query Match
Best Local Similarity 99.9%;
Matches 1498; Conservative
                                ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1923)
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GENERAL INFORMATION:
APPLICANT: Udagawa, Hiroaki
APPLICANT: Tair, Rikako
APPLICANT: Tragi, Shinobu
APPLICANT: Thira, Stic
APPLICANT: Valai, Stic
APPLICANT: Wikeo-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT APPLICATION: WUMBER: US/10/877,849
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
: SEQ ID NO 35
: LENGTH: 1923
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ORGANISM: Artificial
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US-10-877-849-35
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APPLICANT: Udag
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| | 534 AGTICCCAAGACTACTTCCACCGTTCTGTTTCATACAAACTATGAAGATCAGACTCAG 593 421 TCCTCCAGAACTACCACCGTTCTGTTTCTTCATCCAGAACTAGAAGACCAGACCCAG 480 594 GTGAAGATTGCTGGCTAGACTACCAGAACTACGAGACCAGAGCCAGG 480 595 GTTGAAGATTGCTGGCTAGACACACTCTCCTTGCTGATCTCGATACCACAGG 553 [| 774 AAAGCCGCAGGCGTACTGTATCGGCCAGGTGCTCGACGGTGATCCGGCCTACACTTGT 833 | TCCGACTGTCCAGACTCAACACTCCTGGGCACATTCGTCGAGACACGACGACAACCCACGGGGCACTGTCGACTGACT | 1134 CCGGGAACGGAAGCTGCGGGTACCCGACGAGGGGGGGTGTACAAG 1193 |
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| DD TCCGACTGTCCAGACTCCTCGGGGCACATTCGTCGAGAACCCCGCGG 960 1014 TTCGCTTCTTACACCACGACATAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCTCTC 1073 | 1141 | | GENERAL INFORMATION: APPLICANT: Landan, Mike TITLE OF INVENTION: Self-processing Plants and Plant Parts FILE REFERENCE: 109846.317 CURRENT APPLICATION NUMBER: PCT/US02/27129 CURRENT FILING DATE: 2002-10-09 NUMBER OF SEQ ID NOS: 60 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 46 LENGTH: 3285 TYPE: DNA APPE: DNA APPE: DNA APPE: DNA APPE: DNA PORANISM: Aspergillus shirousami PCT-US02-27129-46 | Query Match 58.3%; Score 1011.2; DB 1; Length 3285; Best Local Similarity 81.9%; Pred. No. 7.1e-143; Algabs 0; Gaps 0; Matches 1166; Conservative 0; Mismatches 258; Indels 0; Gaps 0; Qy 114 GCACCCGGCCTGCGGACTGCGCATCCATTATTCCTTCTCTCCTCACGGATCGCTTCGCC 60 0 1 GCACCCGGGCGGCTGCGACTGCTACTACTTCTTCCTCCTCACGGACGCTTCGCC 60 Qy 174 AGGACGGATGGGTCGACGACTGCTACTACTTCTTCTCTCTC |

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                                                                    AAAGCCGCAGGCGTGTACTGTATCGGCGAGGTGCTCGACGGTGATCCGGCCTACACTTGT
                                                                                             661 AAGGCGGCGTGTACTGCATCGCGAGGTGCTCGACGTGGACCCGGCCTACACCTGC
                                                                                                                                                        CCCTACCAGAACGTCATGGACGGGGTACTGAACTATCCCATTTACTATCCACTCCACAAC
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Sequence 46, Application US/10228063
GENERAL INFORMATION:
APPLICANT: Lanahan.
TITLE OF INVENTION: Self-processing Plants and Plant FILE REFERENCE: 10846.317;
CURRENT APPLICATION NUMBER: US/10/228,063;
CURRENT FILING DATE: 2002-12-12;
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 46;
LENGTH: 3285
ILENGTH: 3285
TYPE: DNA
ORGANISM: Aspergillus shirousami
US-10-228-063-46
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                                                                                                                                                        Sequence 46. Application PC/TUS0407182A
GENERAL INFORMATION:
APPLICANT: Lanahan, Mike
TITLE OF INVENTION: Self-processing Plants and Plant Parts
FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: PCT/US04/07182A
CURRENT FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7.1e-143;
0; Mismatches 258; Indels
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PCT-US04-07182A-46
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Best Local Similarity 81.9%;
Matches 1166; Conservative
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Best Local Similarity
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PCT-US04-07182A-46
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LENGTH: 3285
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APPLICANT: Novozymes Biotech, Inc.
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Methods For Aspergillus Niger
FILE REFERENCE: 10345.204-WO
CURRENT APPLICATION NUMBER: PCT/US04/10126
CURRENT FILING DATE: 2004-04-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 17
ACCTACAAGAACTGGCCCATCTACAAAGACGACACAACGATCGCCATGCGCAAGGGCACA 1313
                                                                                                                                              GATGGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACC 1373
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ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10)...(10)
OTHER INFORMATION: n=a,c,g or
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Matches 1609; Conservative
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PCT-US04-10126-17
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                                                                   ACATGGCAGGCATCATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGCCATC
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                                                     GCAACGCCTGCGGACTGGCGATCGCAATCCATTTATTTCCTTCTCACGGATCGATTTGCA
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                            Gaps
  DB 50; Length 3285;
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 Score 1011.2; DB 50; Lengt
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| GTCTCCTTGCCTGATCTCGATACCACCAAGGATGTGGTCAAGAATGAAT | CTGATCGATGATACTTACGAAATCACGTTCCGTATCGACACACGT 74 | | GCTCGACGGGCTACCCCTACTTGTTCCTACCAGAACGTCATGGACGGCGTACTGAA 03 GCTCGACGGTGATCCGGCCTACATGTTCCCCTACCAGAACGTCATGGACGGCGTACTGAA 13 | CTATCCCATGTATGGTTCCTCCAACCATGAGCCTTCTTGCAAGTCTCATCTCCTAACGAA | ACGCTAAAACCAGTTACTATCCACTCCTCAACGCCTTCAAGTCAACCTCCGGCAGCATG | GACGACCTCTACAACATCAACACCGTCAAATCCGACTGTCCAGACTCAAACACTCTGTCCTG | GGCACATICGICGAGAACCACGACAACCCACGGIICGCIIC | 1022TTACACCAACGACA 1035 1591 TTCCGTTCCCAACACACACAGAACCCCACCTAACAAGAGCAAAGTTACACCAACGACA 1650 | 1036 TAGCCCTCGCCAAGAACGTCGCAGCATTCATCATCCTCAACGACGGAATCCCCATCATCT 1095 | 1096 ACGCCGGCCAAGAACAGCACTACGCCGGCGAAACGACCCCGCGAACCGCGAAGCATCT 1155 | 1156 GGCTCTCGGGCTACCCGACCGACGAGCTGTACAAGTTAATTGCCTCCGCGAACGCAA 1215 | 1216 TCCGGAACTATGCCATTAGCAAAGATACAGGATTCGTGACCTACA | 1261 1260 1891 CTAAGCATACCTAATGGCCTATCTTCAGAGTATCTGACACAAGAGACTAATCACTGGCA 1950 | 1261AGAACTGGCCCATCTACAAAGACGACACGATCGCCATGCGCAAGGGCACAGAT 1316 | 1317 GGGTGGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCCTC 1376 2011 GGGTCGCAGATCGTGACTATCTTGTCCAACAAGGGTGCTTCGGGTGATTCGTATACCCTC 2070 | | 1437 ACCGTGACGGTTGGTTCGGATGGAAATGTGCCTGTTCCTATGGCAGGTGGGCTACCTAGG 1496 |
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| TYPE: DNA ORGANISM: Aspergillus niger FEATURE: NAME/KEY: misc_feature LOCATION: (10)(10) OTHER INFORMATION: n=a,c,g or t | Ouery Match 56.5%; Score 979; DB 63; Length 2443; Best Local Similarity 74.4%; Pred. No. 5.1e-138; Matches 1609; Conservative 0; Mismatches 10; Indels 544; Gaps 8; | 5=5 | 61 CGTGGTGGTCTCTATTCTGTACGGCCTTCAGGTCGCGGCACCTGCTTTGGCTGCAACGC 120 | 121 CTGCGGACTGGCGATCGCATCCATTTATTTCCTTCACGGATCGATTTGCAAGGACGG 180 | 181 ATGGGTCGACGACTGCAATACTGCGGATC | 217 | 246 ATCATCGACA 255 451 ATCATCGACAAGGTAAATTGCCCCTTTATCAAAAAAAAAA | | CTTCACAGCCATCTGGATCACCCGGTTACACCAGGGCCCAGGACTAIAICCAGGGGAATGGGCTTACACAGCCCCAGGACCAGACCA | CTICACAGCCATCIGGATCACCCCCGITACAGCCCCAGCIGCCCCAGACCACCCCAACTGCCCAAGCCTACCATGGCTACTGGCAGGATAT | PORTGECTRECT TO THE PROPERTY OF THE PROPERTY CORPORATION OF THE PROPERTY OF TH | A LIGHT | TCTTATGGTCGATGTTGCTACCATAT | 811 TCTTATGGTGGATGGTTGCTAACCATATGGTTGGTGGTGCTTGGAACTGACTTGGGGGGGG | atatggttcafttcagtactgacaatgagtaatatatcagggctatgatggaggggtagc cagtcgattacagtgtgtttaaacgttcagttcccaagactacttccacccgttctgt | 931 TCAGTCGATTACAGTGFGTTTAAACCGTTCAGTTCCCAAGACTACTTCCACCCGTTCTG 990 564 TTCATTCAAAACTATGAAGATCAGACTTCAGGTTGAGATTGCTGGCTAGGAGATAACAT 623 111111111111111111111111111111111111 | GTCTCCTTGCCTGATCTCGATACCACCAAGGATGTGGTCAAGAATGAAT |

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Db 2131 ACCGTGACGCTTGGATGGAAATGTCCCTGTTCCTATGGCAGGTGGCTACCTAGG 2190

Qy 1497 GTATTGTATCCGACTGGAAGGTTGGCAGGTGGAAGGTCGTGAGGGTG 1556

Db 2191 GTATTGTATCCGACTGAGAAGTTGGCAGGTAGATGTAGTAGTAGTCGTGAAGGTG 1556

Qy 1557 GAGAGTATATGATCGAAGTTGGCAGGTAGAAGATTGAACTCGTGAAGGGTG 2250

Qy 1557 GAGAGTATATGATCGTACTGCTATTCAATCTGGCATTGGACAGTTGAATTTGATTTGATC 1616

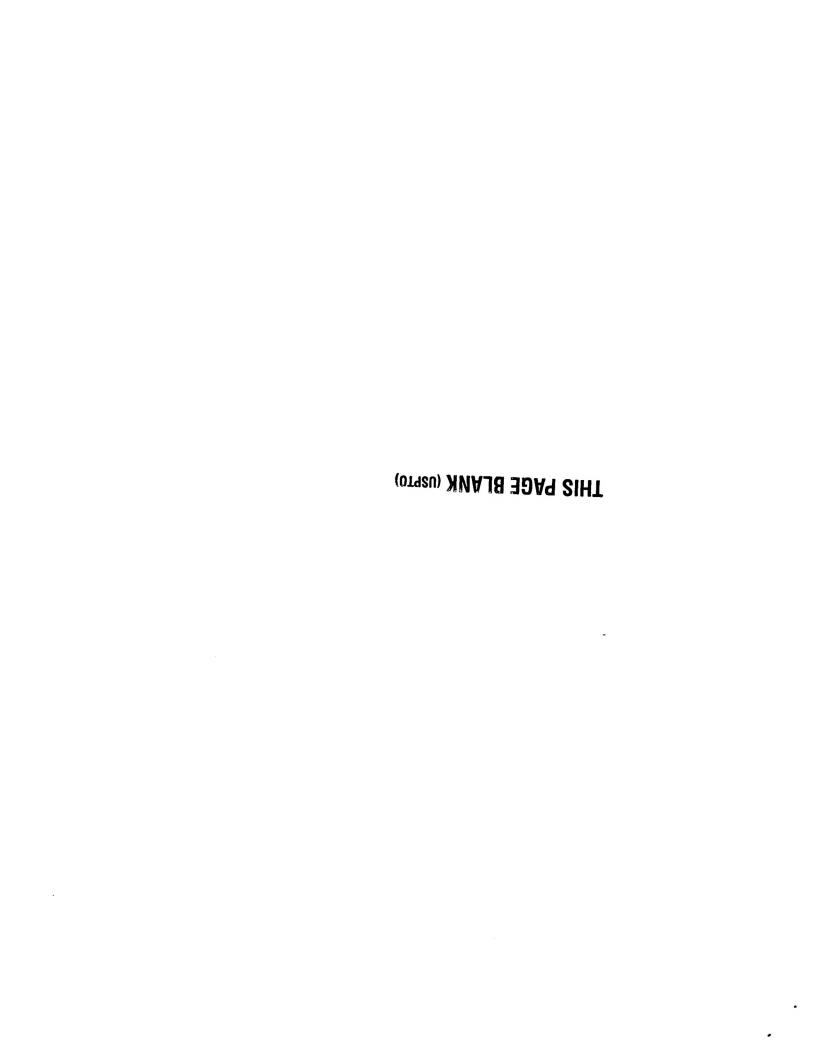
Db 2251 GAGAGTATATGATCGTACTGCTATTCAATCTGGCATTGGACGAGATTGAATTGATC 1616

Oy 1617 TAC 1619

Db 2311 GAC 2313

Search completed: February 12, 2005, 03:41:54

Job time: 6093 Becs
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CCADK28TF AJ638179

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Database

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| Organism="mericella nidulans" | Appe="mRNA" |
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| developmental and vegetative cDNA lambda zap library" |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emericella nidulans (anamorph: Aspergillus nidulans)
Emericella nidulans
Entaryote; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryote; Trichocomaceae; Emericella.

E 1 (bases 1 to 583)

S Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
An Aspergillus nidulans EST Database
L Unpublished (1998)
Cother_ESTs: j4h07al.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
mai. An and Advanced Contact: An Andrean, Norman, OK 73019, USA
            CF718519
CAAA85831
CAAA85831
CAAA86814
AAA86814
CAF697014
AAA85574
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CAC66555
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Pred. No. 1.2e-59;
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High quality sequence stop: 526.
Location/Qualifiers
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AA785147
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AJ638179
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AUTHORS
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CCABA08TR
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CCADW8BTR
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(without alignments)
12620.161 Million cell updates/sec
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AA783132 c1c11a1.r
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- 2005 Compugen Ltd.
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Listing first 45 summaries
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db_xref="taxon:162425"
/clone="hal2al"
/clone="hal2al"
/tissue type="vegetative mycelia, asexual structures"
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Xhol; 5' end of cDNA cloned into ECRI site of pBluescript
3' end of cDNA cloned into Xhol site of pBluescript"
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AA783132 GI:2843300
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Emericella nidulans
Euraryota; Pungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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65.2%; Pred. No. 4.6e-55;
ive 0; Mismatches 188;
                           nidulans"
                         organism="Emericella
                                                /mol_type="mRNA"
/strain="FGSC A26"
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Genetics Stock Center
High quality sequence stop: 510.
Location/Qualifiers
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                                                  TACAACAAAGCCGCAGGCGTGTACTGTATCGGCGAGGTGCTCGACGGTGATCCGGCCTAC
                                                                                             TATATTGATGCCGCTGGGGTCTACAGCGTTGGTGAAATCTTCCATGGGGACCCGGCGTAT
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Gaps
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Department of Chemietry and Blochemietry
Advanced Center foor Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
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Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetės;
Eurotiales; Trichocomaceae; Emericella.
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Prade, R. and Roe, B.
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    Mismatches 202; Indels
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      Conservative
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Fax: 405 325 7762
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var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics, TIGR, 9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="raxon:40410"
/clone="CCAEEB14"
/clone=lib="C.neoformans strain JEC21"
/note="Vector: pCNVSport6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"
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                                                                                                                         Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
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/mol_type="mRNA"
/strain="JEC21"
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Pred. No. 1.4e-50;
0; Mismatches 378;
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Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
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JEC21 cDNA library
Unpublished (2003)
Other_EST8: CCAEE14TO
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Seg primer: TR.
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                                                                                               Unpublished Contact: Description of Contact: Unpublished Contact: Bruce A. Roe, University of Oklahoma, broegou.edu
Contact: Bruce A. Roe, University of Oklahoma, broegou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4762
Email: broegou.edu
Fax: 405 325 7762
Email: broegou.edu
We anticipate the future release of the CDNA clones to the Fungal
Genetics Stock Center
Seq primer: SK
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Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
Prade,R. and Roe,B.
An Aspergillus nidulans BST Database
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/clone_lib="Aspergillus nidulans 24hr asexual
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Pred. No. 1.9e-51;
0; Mismatches 148; Indels 0
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    .561
    /organism="Emericella nidulans"

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Matches 316, Conservative
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

1 (bases 1 to 464)
Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
                                                                                                                                                                                                                                                                                                                              CCCCCGTTACAGCCCAGCTGCCCCAGACCACCATATGGAGATGCCTACCATGGCTACT
                                                            Emericella nidulans (anamorph: Aspergillus nidulans)
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/db_xref="taxon:40410"
/clone="CQAEG51"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pcMvSport6; Site 1: NotI_EcoRV; The full
/note="Vector: pcMvSport6; Site 1: NotI_EcoRV; The full
/note="vector: pcMvSport6; Site 1: NotI_EcoRV; The full
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Heterobasidiomycetes; Tremellomycetidae; Tremellales;
Filobasidiella.
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Pred. No. 1.4e-47;
0; Mismatches 361; Indels
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JEC21 cDNA library
Unpublished (2003)
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Rockville, MD 20850, USA
Tel: 301-838-3543
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CF711819.1 GI:41565978
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TIGR
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Best Local Similarity 55.4%;
Matches 456; Conservative
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Loftus, B.
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CF711819
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SOURCE
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neoformans (Filobasidiella neoformans

neoformans var.

9712 Medical Center Drive,

Genomics, TIGR,

Eukaryotic

Mon

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End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library Unpublished (2003) Other_ESTS: CCABA08TF
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Cryptococcus neoformans var. neoformans"
                                                                              Eukaryota, Fungi, Basidiomycota, Hymenomycetes,
Heterobasidiomycetes, Tremellomycetidae, Tremellales,
                                           var. neoformans)
Cryptococcus neoformans var. neoformans
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .779
                                                                                                                                                                                                                                                                                          Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@eigr.org
Seq primer: TR.
                                                                                                                                                                                                                                              Contact: Brendan Loftus
                                                                                                                                 (bases 1 to 779)
                                                                                                                    Filobasidiella.
                                                                                                                                                                                                                                                                                  Department of Rockville, MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCACTCCTCAACGCCTTCAAGTCAACCTCCGGCAGCATGGACGACCTCTACAACATGA
Prade, R. and Roe, B.

An Aspergillus nidulans EST Database
Unpublished (1998)
Contact: Bruce A.

Gontact: Bruce A.

Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Fal: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
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                                                                                                                                                                                                                       Seg primer: T3
High quality sequence stop: 453
Location/Qualifiers
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Best Local Similarity 65.9%;
Matches 305; Conservative
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/mol type="mmNA"
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                                                                                                                                                                                                                                                                                                                                                                                                             7
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nes 430; Conserv
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CF705447 C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCABA08, mRNA sequence.
CF705447.1 GI:41559606

LOCUS

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CF709355 75.4 Dp mRNA linear EST 16-AUG-2004 CCAA414TR C.neoformang strain JEC21 Cryptococcus neoformang var. neoformang cDNA clone CCAA414, mRNA sequence.
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Cryptococous neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
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/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSport6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
428
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                                                                                         249 ATCGACAAGTTGGACTATATCCAGGGAATGGGCTTCACAGCCATCTGGATCACCCCCGTT 308
                                                                                                                                                     283
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                                                                                                                            369 GATATATACTCTCTGAACGAAAACTACGGCACTGCAGATGACTTGAAGGCGCTCTCTTCG
                                                                                                                                                                                                                                                                                                                                                                                          344 AACATATACGGTGTCGACACCACCACGACACACCCGACGATATCAGGGCTCTGTCGGAG
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1. .753
1. .753
2. Coganism="Cryptococcus neoformans" /mol type="mRNA" /mol type="mRNA" /mol type="mRNA" /mol type="mRNA"
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56.1%; Pred. No. 1.9e-39;
ive 0; Mismatches 285; Indels
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Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.
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Best Local Similarity 56.1
Matches 368; Conservative
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/clone="o6c07a1"
/tlssue type="vegetative mycelia, asexual structures"
/clone lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/note="vector: pBlueScript SK-; Site_1: EOCR!; Site_2:
Xhol; 5, end of cDNA cloned into ECORI site of pBluescript
3, end of cDNA cloned into Xhol site of pBluescript
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   ACTTGAACACTGAGAGTGACACTGTTGTTTCTTACTGGAACCAATGGATCACAGACCTTG 544
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

1 (bases 1 to 466)
Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe, B.

4 n Aspergillus nidulans EST Database
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other BST8: o6c07a1.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Pax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   874 TITACTATCCACTCCTCAACGCCTTCAAGTCAACCTCCGGCAGCATGGACGACCT 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: broegou.edu
We anticipate the future release of the cDNA clones to the
Genetics Stock Center
Seg primer: T3
High quality sequence stop: 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           · 0
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/strain="FGSC A26"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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Cryptococcus neoformans var. neoformans
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Heterobasidiomycetes; Tremellaceae;
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         / strain="JECINTA"
/ db xref="taxon:40410"
/db xref="taxon:40410"
/clone="CCAAM6"
/clone=lib="C.neoformans strain JEC21"
/note="Vector: pCMVSport6; Site_1: Not1 EcoRV; The full length, normalized library was prepared from a variety conditions using RNA provided by Joseph Heitman and Jennifer Lodge"
                                                                                                                                                                                                                                                                  CTGCGGACTGGCGATCGCAATCCATTTATTTCCTTCTCACGGATCGATTTGCAAGGACGG
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                                                                                                                                                      CCCCCGTTACAGCCCAGCTGCCCCAAGACCACCGCATATGGAGATGCCTACCATGGCTACT 360
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CCAAM64TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAAM64, mRNA sequence.
                ATGGGTCGACGACTGCGACTTGTAATACTGCGGATCAGAAATACTGTGGGAGCACATGGC
                                                                                                         213 CCGCTCTCGCCGACAACTCGACTATATTCAGGGAATGGGCTTTGACACTGTCTGGATAT
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Heterobasidiomycetes; Tremellomycetidae; Tremellales;
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Rockville, MD 20850, USA
Tel: 301-838-3543
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CP679247.1 GI:41533406
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Email: crypt@tigr.org
Seq primer: TR.
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1 (bases 1 to 783)
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Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellaceae;
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/strain="uBC21"
/db_xrel="taxon:40410"
/db_xrel="taxon:40410"
/clone="cCAGT90"
/clone lib="C.neoformans strain JEC21"
/note="vector: pCVNSport6; Site 1: NotI_EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and
                                                                                                                                                         CF687484 13 T6-AUG-2 CCAGT90TR C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans cONGT90, mRNA sequence.
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1. .762
/organism="Cryptococcus neoformans var. neoformans"
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                      721 TCCGTATCGACACAGTAAAACACGTCCAGAAGGACTTCTGGCCCG
                                               701 TTTCGATTGATACCGTCAAGCATGTTCGTCAATCTTTCTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Greckville, MD 20850, USA Tel: 301-838-3543 Fax: 301-838-0208 Email: crypt@rigr.org Seg primer: TR.
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Unpublished (2003)
Other_EST8: CCAGT90TF
Contact: Brendan Loftus
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1 (bases 1 to 762)
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/clone="CCAAQ16"
/clone=lib="C.neoformans strain JEC21"
/clone_lib="C.neoformans strain JEC21"
/clone_lib="Vector: pCMVSport6; Site_1: NotI_EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                         End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library Umpublished (2003) Other ESTS: CCAAQ13F Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGTICTICATTGCACGCCAGGGGAATGTACCTCCAGGTCGACGTCGTCGTTAACCACG
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                                                                                                                                                                                                                                                                                                                                     1. 764
Corganisma="Cryptococcus neoformans var."
/mol type="mkNa"
/strain="JEC21"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                            Department of Bukaryotic Ge
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.
                                      (bases 1 to 764)
                    Filobasidiella
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Eukaryota, Fungi, Basidiomycota, Hymenomycetes,
Heterobasidiomycetes, Tremellomycetidae, Tremellales, Tremellaceae,
                                                                                                                                           177 AGAACCTCTACTGCGGAGGATCATGGAGGGGCATAATCAGCAAGTTGGACTATATTAAAG 236
                                                                                                                                                                                                                                                                                                      Genomics, TIGR, 9712 Medical Center Drive,
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/note="Vector: pCMVSport6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
    57 TCGCCGGACTAGCATTAGCAGCGGACACCGTCGATTGGAAATCCAGGTCGATATATCAGG 116
                                                                                                                                                                                                                                        237 AAATGGGCTTCGATGCCATCATGATCTCACCAGTCTCGAAAATGTCGAAGGTCGCGTTA 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF691968 798 bp mRNA linear EST 16-AUG-21 CCADW88TR C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans clone CCADW88, mRNA sequence.
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                                                                   214 ATCAGAAATACTGTGGTGGAACATGGCAGGGCATCATCGACAAGTTGGACTATATCCAGG
                                           154 TICTCACGGATCGATTTGCAAGGACGGATGGGTCGACGACTGCGACTTGTAATACTGCGG
                                                                                                                                                                                                                                                                                 334 CATATGGAGATGCCTACCATGGCTACTGGCAGCATATATACTCTCTGAACGAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         454 TTATGGTCGATGTGGTTGCTAACCATATGGGCTATGATGGAGCGGGTAG-----
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Cryptococcus neoformans var. neoformans
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/clone="CCADW88"
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Rockville, MD 20850, USA
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Unpublished (2003)
Other EST8: CCADW88TF
Contact: Brendan Loftus
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EST.
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Tel: 301-838-3543
Fax: 301-838-0208
Emall: crypt@tlgr.org
Seq primer: TR:
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/clone lib="Mycelium and yeast cells from Paracoccidioides
brasilTensis"
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                                                                                                                                                                                               GATTGCTGGCTAGGAGATAACACTGTCTCCTTGCCTGATCTCGATACCACCAAGGATGTG 659
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                                                                                                                                                                                                                                                                                                                                                                                  694 ATTCGAATTGATACCGTCAAGCATGTTCGTCAATCTTTCTGGACAGATTTCGTCAACGCT 753
TGAGTICTICATIGCACGCCAGGGAATGTACCTCCAGGTCGACGTCGTCGTTAACCACG 453
                                                                                                                                                                                                                                      574 caarierriederriedercacricitercarririedeceacricaacacricadercacr 633
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                                       TGGCTATGATGGAGCGGGTAGCTCAGTCGATTACAGTGTGTTTAAAACCGTTCAGTTCCC
                                                                              454 icecreccacercraerreracerrecaacerrecaarerracegreerrracairacrr
                                                                                                                     541 AAGACTAC-TTCCACCCGTTCTGTTTCATTCAAAACTATGAAGATCAGACTCAGGTTGAG
                                                                                                                                                          514 CTGAAGACATACCACCCTTTCTGCTGGATCACTGACTACAACAACCAGACCAACGTTGAG
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Institute of Biology - University of Brasilia
Campus Universitario, Asa Norte, Brasilia, DF 70910-900, BRA
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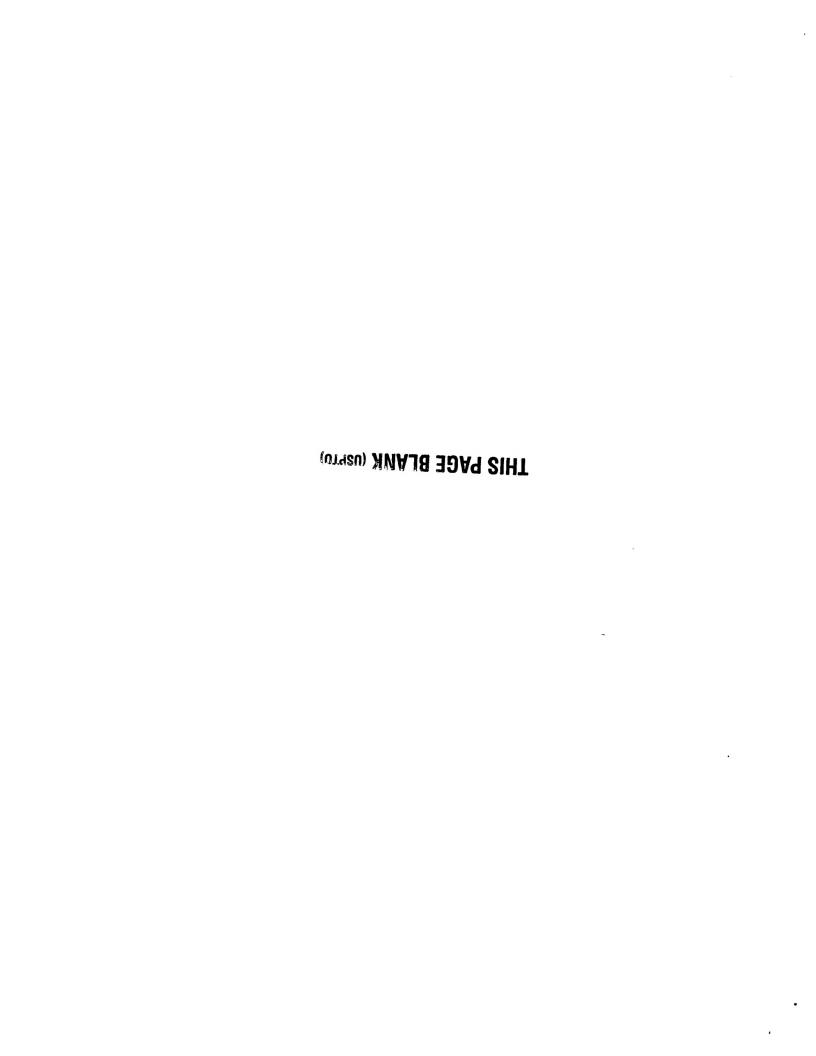
    .589
    /organism="Paracoccidioides brasiliensis"

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Paracoccidioides brasiliensis
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/strain="Pb01"
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Fax: 55 61 349 8411
Email: msueli@unb.br
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EST 16-AUG-2004

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sequencing of clones from a Full length enriched, normalized
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                                                                                                                                                                                         Location/Qualifiers
                                                                                        Department of Eukaryotic Ge
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@rigr.org
Seq primer: TR.
      JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCAHO40TF
Contact: Brendan Loftus
                                                                                                                                                                                                          . .865
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Cryptococcus neoformans var. neoformans
Cryptococcus neoformans var. neoformans
Bukaryota; Busidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellacese;
Filobasidiella.
Filobases I to 865)
Loftus, B.
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                                                                                               Gaps
   and
conditions using RNA provided by Joseph Heitman
Jennifer Lodge"
                                                                                             3,
                                                                798;
                                                            Score 166.2; DB 7; Length
Pred. No. 1.7e-34;
0; Mismatches 308; Indels
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Best Local Similarity 53.9%;
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/clone="CCAHO40"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCWVSport6; Site_1: NotI_ECoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"
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9712 Medical Center Drive,
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/mol_type="mRNA"
/strain="JEC21"
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Genomics, TIGR,
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US-08-720-899-7
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Sequence 22820, Appli
Sequence 4442, Appli
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49989, A
                                                                                                                             8, 2005, 18:29:19; Search time 1.08108 Seconds (without alignments) 483.353 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-10404
US-09-328-352-4170
US-09-270-767-34772
US-09-270-767-49989
US-09-198-452A-924
US-09-0438-185A-858
US-09-081-385-148
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                          US-10-820-200-2_COPY_161_167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                 Run on:
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28 30 75.0 25 10.00-48-25-11 Sequence 41, Appl 21 30 75.0 25 2 10.00-48-210-41 Sequence 41, Appl 21 30 75.0 25 2 10.00-41-48-110-41 Sequence 41, Appl 21 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 21 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 21 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 31 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 31 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 31 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 31 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 31 30 75.0 25 3 10.00-47-411-41 Sequence 41, Appl 31 30 75.0 6 25 3 10.00-47-411-41 Sequence 41, Appl 41 30 75.0 6 42 10.00-47-411-41 Sequence 41, Appl 41 30 75.0 6 42 10.00-47-411-41 Sequence 41, Appl 41 30 75.0 6 42 10.00-47-411-41 Sequence 41, Appl 41 30 75.0 6 42 10.00-47-411-41 Sequence 75, Appl 41 30 75.0 6 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-411-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Sequence 75, Appl 42 10.00-47-41 Se
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E: No. 58308370 No. 5830837disk of No. 5830837th America, Inc. 405 Lexington Avenue, 64th Floor
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APPLICANT: Takada, Toshikazu
APPLICANT: Shimada, Jiro
APPLICANT: Shimada, Jiro
APPLICANT: Shimada, Jiro
APPLICANT: Kuriki, Takashi
APPLICANT: Yanase, Michiyo
APPLICANT: Yanase, Hiroki
APPLICANT: Takata, Hiroki
APPLICANT: Orakada, Shigeraka
TITLE OF INVENTION: NEUPULLULANASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
STREET: Metropolitan Square Building, Suite 800, 1450
STREET: G. Street
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 2; Length 478; 100.0%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                    COUNTRY: USA

ZIP: 10174-641

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY DE., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COCKET NUMBER: 31,274
REFERENCE/COMMUNICATION INFORMATION:
TELEFAX: 212-867-0123
INFORMATION FOR SEQ ID NO: 7:
SEGUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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APPLICATION NUMBER: JP 306096/1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08339715A Patent No. 5965442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 SSODYFH 147
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                                                   New York
New York
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       ADDRESSEE: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20002
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APPLICANT: Biggaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB 1; Length 478; 100.0%; Pred. No. 4.7; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITALE: New York
STATE: New York
COUNTRY: USA
ZIP: NOI14-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PE PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08343804
Patent No. 5830837
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Mariame
APPLICANT: Van der Zee, Pia
TILLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                     RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. S801043
; Patent ThroRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lowney Dr., Karen A. REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 40:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-878-9655
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
                                                     141 SSODYFH 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SSQDYFH 7
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US-08-343-804-7
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Gaps

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ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
STREET: 405 Lexington Avenue, 64th Ploor
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Pred. No. 4.7;
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CITY: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Roppy disk
COMPUTER: 1BM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
F1LING DATE:
CLASSIFICATION:
RRICH APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908
FILING DATE:
APPLICATION NUMBER: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REFERENCE/DOCKET NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 322-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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FILE REFERENCE: 4796,204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
                                                                                                                                                                                                                                          APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Toxben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                            Sequence 10, Application US/08683838A Patent No. 6022724 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1996-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                 141 SSODYFH 147
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STRANDEDNESS: si
    1 SSQDYFH 7
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Patent No. 5989169
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: United States of America
ZID: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 38,475
TELEPRAK: 212-67-0123
TELEPRAK: 212-67-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 40; DB 2
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches
                                                                                                   18335.009
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Melser, Allen;
REGISTRATION NUMBER: 27,215
REFRENCE/DOCKET NUMBER: 1833;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-824-8000
TELEPAK: 202-824-8199
                                                                                                                                                                                          TELEX: 248516
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-715A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
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Gaps

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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION UNMER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torban
APPLICANT: Borchert, Torban
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796-204-08
FILE REFERENCE: 4796-204-08
FILE REFERENCE: 4796-204-08
FRIOR APPLICATION NUMBER: US/09/672,459
FRIOR APPLICATION NUMBER: 09/182,859
FRIOR APPLICATION NUMBER: 09/182,859
FRIOR APPLICATION NUMBER: 09/182,859
FRIOR FILING DATE: 1996-10-29
FRIOR FILING DATE: 1996-06-28
FRIOR FILING DATE: 1996-06-28
FRIOR FILING DATE: 1996-06-28
FRIOR FILING DATE: 1996-07-30
FRIOR FILING DATE: 1996-07-31
FRIOR FILING DATE: 1996-07-31
FRIOR FILING DATE: 1996-07-31
FRIOR FILING DATE: 1996-07-31
FRIOR FILING DATE: 1996-07-31
FRIOR FILING DATE: 1996-07-31
FRIOR FILING DATE: 1996-37-31
FRIOR FILING DATE: 1996-37-31
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FRIOR FILING DATE: 1996-37-31
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   CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-248-796A-22820
; Sequence 22820, Application US/09248796A
; Patent No. 6747137
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                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SSQDYFH 7
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Patent No. 6440716
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE REPRENCE: 0776/1F214-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bagard-Frantzen, Henrik
TITLE OF INVERTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION WUMBER: US/09/672,459
CURRENT APPLICATION WUMBER: 09/182,859
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASELSEQ FOR WINDOWS VERSION 3.0
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER PILING DATE: 1996-07-11
; EARLIER FILING DATE: 1996-07-11
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7;
; LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09672459
Patent No. 643688
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bacillus licheniformis
US-09-182-859-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-636-252A-10
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US-09-672-459-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 478
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                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Sequence 21, Application US/08700359

Patent No. 5765925

GENERAL INFORMATION:
APPLICANT: SUGINOTO, MASAKAZU
APPLICANT: SUGINOTO, MASAKAZU
APPLICANT: TANAKA, AKTKO
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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32;
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                                                               FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATINIGID., Pamela Deneke
NEGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 32; DB 100.0%; Pred. No. 32; Live 0; Mismatches
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...95
SEQUENCE DESCRIPTION: SEQ ID NO: 4442:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: ISM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 08-OCT-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-35019
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4442:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 ODYFH 55
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i Sequence 4016, Application US/09583110

i Patent No. 6699703

i GENERAL INVENTATION:

I TILLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

I TILLE OF INVENTION: Denumentae for Diagnostics and Therapeutics

I TILLE OF INVENTION: Denumentae for Diagnostics and Therapeutics

I TILLE OF INVENTION: Denumentae for Diagnostics and Therapeutics

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR PAPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4016
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US-09-107-433-4442
; Sequence 4442, Application US/09107433
; Patent No. 6800744
; Patent No. 680074410N:
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: THERAPEUTICS
                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                        Score 33; DB 4; Length 180;
Pred. No. 40;
1; Mismatches 0; Indels
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28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22820
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pneumoniae US-09-583-110-4016
                                                                                                                                                                                                            82.5%;
                                                                                                                   TYPE: PRT;
; ORGANISM: Candida albicans
US-09-248-796A-22820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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Best Local Similarity 83.3
Matches 5; Conservative
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102 NQDYFH 107
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                                                                                               Score 32; DB 1; Length 369;
Pred. No. 1.3e+02;
1; Mismatches 1; Indels
        10-819-0 PCT
      REFERENCE/DOCKET NUMBER: 10-8:
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-2200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
REGISTRATION NUMBER: 24,618
                                                                                                Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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133 SSMDYYH 139
                                                                         TOPOLOGY: linear
                                                                                                                                1 SSQDYFH 7
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; CLONE: 496071
US-08-616-392C-4
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Sequence 4124, App Sequence 496, App Sequence 72639, A Sequence 42805, App Sequence 42805, App Sequence 75391, A Sequence 75391, A Sequence 75311, A Sequence 1162, App Sequence 1162, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1184, App Sequence 1281, App Sequence 1281, App Sequence 1281, App Sequence 1281, App Sequence 1281, App Sequence 1281, App Sequence 1281, App Sequence 1281, App Sequence 1281, App

Sequence 1281, Sequence 1682, Sequence 1754, Sequence 1998, Sequence 2036,

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Query Match
100.0%; Score 40; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels
0 US-09-970-944-20

5 US-10-424-599-162174

7 US-10-472-928-49124

7 US-10-282-122A-72639

US-09-924-659-162174

US-09-924-659-162174

US-09-924-659-1079

US-09-924-65-1079

US-10-282-122A-74836

5 US-10-282-122A-74836

5 US-10-282-122A-74836

5 US-10-282-122A-74836

5 US-10-282-122A-74836

6 US-10-283-136212

4 US-10-437-968-1866

US-09-984-245-184

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US-09-796-692-1754
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US-10-040-862-1682
US-10-040-862-1754
US-10-040-862-1998
US-10-040-862-2036
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Sequence 10, Application US/10184771
Sequence 10, Application US/10184771
Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequ
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US-10-186-042-7
; Sequence 7, Application US/10186042
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    TYPE: PRT
    ORGANISM: A. oryzae
US-10-184-771-10
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    1 SSODYFH
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140941,
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                                                                                                                                                              8, 2005, 18:42:07; Search time 3.01351 Seconds (without alignments) 756.564 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBGOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBGOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
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| cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.ppp:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-186-042-7
US-10-926-720-10
US-10-915-495-22
US-10-815-495-18
US-10-228-63-45
US-10-228-63-45
US-10-228-63-16
US-10-424-599-218859
US-10-424-599-218859
US-10-424-963-14-9641
US-10-427-963-14-9641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   1373511 seqs, 325702437 residues
                                                                                                                                                                                                                                                               US-10-820-200-2_COPY_161_167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                   February
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Perfect score:
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141 SSQDYFH 147
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100.0%; Score 40; DB 15;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0;
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JOS-10-0344-18-7.

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JOSCHORAN TION:

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JOSCHORAN TO SUCHER, TORDEN

APPLICANT: BISGRACFFRANTSEN, HENRIK

FILE REFERENCE: 4796.204-US

CURRENT APPLICATION NUMBER: US/10/644,187

CURRENT FILING DATE: 2003-08-20

PRIOR PILING DATE: 1996-06-29

PRIOR PILING DATE: 1996-04-30

PRIOR FILING DATE: 1996-07-11

PRIOR PILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-07-11

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PRIOR FILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-07-11

PRIOR PRIOR DATE: 1996-07-11
                                                 GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bargard-Frantzen, Henrik
APPLICANT: Blagard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION WUMBER: US/09/672,459
FRIOR APPLICATION NUMBER: US/09/672,459
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRSESQ FOR WINDOME Version 3.0
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; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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      Publication No. US20030171236A1
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GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Meriads
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REPERENCE: 10345,200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                       ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                       APPLICANT: Svendsen, Allan
Bisg+rd-Frantzen, Henrik
Borchert, Torben Vedel
TITLE OF INVENTION: -Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
US-10-926-720-10
; Sequence 10. Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/10815495
Publication No. US20040191864A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 478 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
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Gaps

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0; Indels

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US-10-424-599-175172
US-10-424-599-175172
Sequence 175172, Application US/10424599
Publication No. US20040031072A1
SEQUENCE 175172, Application No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223)
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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                                                               Sequence 16, Application US/10298638
Publication No. US20030177527A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPONENTS IN DURABLE AND BROAD-RANGE RESISTANCE
TITLE OF INVENTION: COMPONENTS IN DURABLE AND BROAD-RANGE RESISTANCE
TITLE OF INVENTION: COMPONENTS IN DURABLE AND BROAD-RANGE RESISTANCE
TITLE OF INVENTION: STRATEGIES BASED ON PLANT DEFENCE
FILE REFERENCE: 2121-0167P
CURRENT APPLICATION NUMBER: US/10/298,638
CURRENT FILING DATE: 2002-11-19
PRIOR FILING DATE: 2002-11-19
SPRIOR FILING DATE: 2002-11-19
SEQ ID NOS: 26
SOFTWARE: PATENTING OF SECTION NOS: 26
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_129199C.1.pep
US-10-424-599-175172
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Pred. No. 98;
1; Mismatches 0
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175172
LENGTH: 133
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US-10-298-638-16
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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98 SEDYFH 103
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US-10-228-063-45
; Sequence 45, Application US/10228063
; Sequence 45, Application No. US2030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENCTH: 1095
                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB 16; Length 498; 100.0%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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; ORGANISM: Aspergillus shirousami
US-10-228-063-45
SOFTWARE: PatentIn version 3.2 SEQ ID NO 22
                                                                                                     ; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Aspergillus niger
US-10-815-495-18
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 SSQDYFH 168
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 SSQDYFH 168
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LENGTH: 499
TYPE: PRT
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APPLICANT: Harrman, John L
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: No. US20030204052Alel Proteins and Nucleic Acids Encoding Same and
TITLE OF INVENTION: Antibodies Directed Against these Proteins
FILE REFERENCE: 21402-138
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/237,862
PRIOR APPLICATION NUMBER: 60/237,862
PRIOR PLING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 4351
                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-65668

US-10-425-114-65668, Application US/10425114

Sequence 65668, Application WS/10425114

Publication No. US20040034888A1

Sequence 10 US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Danks and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Danks and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 65668

LENGTH: 703
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Pred. No. 5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                     Length 193;
                                                                                                                                                                                                                    0; Indels
                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_42092C.1.pep
US-10-437-963-140941
                                                                                                                                                                h 82.5%; Score 33; DB 16; Similarity 71.4%; Pred. No. 1.4e+02; 5; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: 700333159_FLI.pep
US-10-425-114-65668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09970944; Publication No. US20030204052A1; GENERAL INFORMATION:
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; ORGANISM: Rattus norvegicus
US-09-970-944-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                           TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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138 SAKDYFH 144
                                                                                                                                                                                         Best Local Similarity
Matches 5; Conserve
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82 SEDYFH 87
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ORGANISM: Zea mays
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    LENGTH: 193
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**Sequence 140941, Application US/10437963

**Publication No. US20040123343A1

**GENERAL INFORMATION:

**APPLICANT: La Rosa, Thomas J.

**APPLICANT: Shou, Yihua

**APPLICANT: Cao, Yongwei

**APPLICANT: Too, Yongwei

**APPLICANT: Buckharov, Andrey A.

**APPLICANT: Barbazuk, Brad

**APPLICANT: Li, Ping

**TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

**ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

**TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

**FILE REFERENCE: 38-21(53221)

**CURRENT APPLICATION NUMBER: US/10/437,963

**CURRENT PLING DATE: 2003-05-14

**NUMBER OF SEQ ID NOS: 204966

**SEQ ID NO 140941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-767-701-39199

| Sequence 39199, Application US/10767701
| Publication No. US20040172684A1
| Publication No. US20040172684A1
| GENERAL INFORMATION:
| APPLICANT: Kovalic, David K.
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| FILE REPERENCE: 38-21(53535) B
| CURRENT APPLICATION NUMBER: US/10/767,701
| CURRENT FILING DATE: 2004-01-29
| NUMBER OF SEQ ID NOS: 63128
| SEQ ID NOS: 63128
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLE REFERENCE: 38 21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 155
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                                                                                                                                                                                                                                                                                                               Score 33; DB 15; Length 155;
Pred. No. 1.1e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C99243_1.pep
US-10-767-701-39199
                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_39658C.1.pep
US-10-424-599-218859
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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ORGANISM: Sorghum bicolor
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ORGANISM: Glycine max
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112 SAKDYFH 118
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7 SARDYFH 13
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Best Local Similarity
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RESULT 15
US-10-444-599-162174

1 Sequence 162174, Application US/10424599

2 Fquence 162174, Application US/10424599

3 Fquence 162174. Application No. US2004003107241

3 FPLICANT: La Rosa Thomas J

4 APPLICANT: Kovalic David K

5 APPLICANT: Aco Yongwei

7 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

7 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

7 TITLE OF INVENTION: 138-21(53223)

8 CURRENT APPLICATION NUMBER: US/10/424,599

7 CURRENT APPLICATION NUMBER: US/10/424,599

8 CURRENT APPLICATION NUMBER: US/10/424,599

8 CURRENT APPLICATION NUMBER: US/10/424,599

9 CURRENT APPLICATION NUMBER: US/10/424,599

9 CURRENT APPLICATION NUMBER: US/10/424,599
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Query Match 82.5%; Score 33; DB 10; Length 4351; Best Local Similarity 71.4%; Pred. No. 3e+03; Matches 5; Conservative 1; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.0%; Score 32; DB 15; Length 71; Best Local Similarity 83.3%; Pred. No. 82; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117460C.1.pep
US-10-424-599-162174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
                                                                                                                                    : |||||
605 NEQDYFH 611
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21 SKDYFH 26
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Protein e Mature Er

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Erwinia c Transcrip Human PAN Novel hum Tumour-as

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Novel

Adr95807 Abb00681 Adm92084 Abb28341 Abb28341 Abb28341 Abb98616 Abb98616 Abb7881 Abg15126 Abg15126 Abg72922 Abg72922 Abg72922 Abg72923 Abg72938

pnenmo

Novel Human

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ABU44715
ABP98616
                                            ABB70891
AAW26654
ABG72922
ABM81509
ADP25358
AAB56501
                                                                     ADK62434
AAY33673
AAM79737
                                    ADO61605
ABG15126
                    ADH45430
                                 ABP98615
2005, 18:22:38; Search time 4.01351 Seconds (without alignments) 674.552 Million cell updates/sec
   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                           US-10-820-200-2_COPY_161_167
                    OM protein - protein search, using sw model
                                                                Gapop 10.0 , Gapext 0.5
                            8,
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                            February
                                                             BLOSUM62
                                            Title:
Perfect score:
                                                            Scoring table:
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ALIGNMENTS

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

0B 0B

Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

2105692 segs, 386760381 residues

Searched:

Sequence:

Run on:

Human pro Disease t B. bassia B. bassia Human pro

PRO polyp

Thermus sp. 1M6501; maltogenic amylase; EC 3.2.1.133; crystallisation; protein co-ordinate data; 3 dimensional structure. Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization. Aspergillus oryzae TAKA protein (TAA) ABB09072 standard; protein; 423 AA 99KR-00039130. 99KR-00039130 (POST-) POSTECH FOUND. (SAMY-) SAMYANG GENEX CORP. (first entry) WPI; 2001-534477/59. Aspergillus oryzae Kim TJ, Park GH; KR2001027418-A. 09-SEP-1999; 09-SEP-1999; 26-JUN-2002 06-APR-2001. RESULT 1 ABB09072

Disclosure; Page 188; 196pp; Korean.

3.2.1.133) having improved transplaces of the comprising many and any analysis. Manufacturing maltogenic amylase comprises the following steps: crystallisation and the three dimensional structure of maltogenic amylase comprises the following steps: (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid pUC119 to construct recombinant DNA (pThMAI19); (ii) inserting the recombinant DNA to Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsus for 10 hours in Luria Bertani (LB) media and centrifuging the media to obtain a microbial cell; (iii) suspending the microbial cell; (iii) suspending the microbial cell with buffer solution at pH 7.5 and obtaining supernatant; and (1v) passing the supernatant through column chromatography and obtaining purified maltogenic amylase is a dimer comprised of two The present invention describes manufacturing maltogenic amylase (BC

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prihted, and is derived by analysis of the total score distribution.

geneseqp1980s: *
geneseqp1990s: *
geneseqp2000s: *
geneseqp2001s: *
geneseqp201s: *
geneseqp201ss: *
geneseqp2003ss: *
geneseqp2003bs: *

A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseσm1990r.*

Database

| | • | مه | | | SUMMARIES | • |
|---------------|-------|-------|-----------|------------|-----------|--------------------|
| Result No. | Score | Query | Length DB | DB | ΙD | Description |
| | 40 | 100.0 | 423 | 4 | ABB09072 | Abb09072 Aspergill |
| 7 | 40 | 100.0 | 478 | ~ | AAR46065 | Aar46065 Mutant al |
| m | 40 | 100.0 | 478 | ~ | AAR72450 | Aar72450 Aspergill |
| 4 | 40 | 100.0 | 478 | ~ | AAR78270 | Aar78270 Aspergill |
| S | 40 | 100.0 | 478 | 7 | AAR79025 | Aar79025 Mature ta |
| 9 | 40 | 100.0 | 478 | ~ | AAW14500 | Aaw14500 Aspergill |
| 7 | 40 | 100.0 | 498 | 4 | AAB84206 | Aab84206 Amino aci |
| 80 | 40 | 100.0 | 498 | æ | ADT89632 | Adt89632 Aspergill |
| σ | 40 | 100.0 | 499 | 6 0 | ADT89628 | Adt89628 Aspergill |
| 10 | 40 | 100.0 | 1095 | 9 | ABP96630 | Abp96630 Alpha-amy |
| 11 | 37 | 92.5 | 493 | ~ | AAR88212 | |
| 12 | 34 | 85.0 | 52 | 4 | AA008447 | |
| 13 | 34 | 85.0 | 1222 | ო | AAG36453 | - |
| 14 | 34 | 'n | 1257 | m | AAG36452 | - |
| 15 | 34 | 85.0 | 1275 | m | AAG36451 | Aag36451 Arabidops |
| 16 | 33 | 82.5 | 116 | S | ABP08801 | |
| 17 | 33 | 82.5 | 124 | 4 | AA005772 | |
| 18 | 33 | 82.5 | 342 | 9 | ABU70873 | Abu70873 Human adi |
| 19 | 33 | 82.5 | 379 | 8 | ADO58298 | Ado58298 S. domunc |
| 20 | 33 | 82.5 | 2112 | 7 | ADG76988 | Adg76988 Human nuc |
| 21 | 33 | 82.5 | 3124 | ω | ADJ78494 | Adj78494 ElA bindi |
| 22 | 33 | 82.5 | 4351 | 7 | ADG42622 | Adg42622 Rat MEGF1 |
| 23 | 32 | 80.0 | 82 | œ | ADN05042 | Adn05042 Antipsori |
| 24 | 32 | 80.0 | 82 | æ | ADP25302 | Adp25302 PRO polyp |
| 25 | 32 | 80.0 | 84 | æ | ADK47501 | Stre |

141 SSÓDYFH 147

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1 SSQDYFH 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low ph. The enzyme can be used as an additive for detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
 maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase
             (ThMA) crystal. The amylase has a structure containing an activated region that consists of amino acid residues of Asp-328, Glu-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn131, Glu1332, Val1329, and His1360. The present sequence represents Aspergillus oryzae TAKA protein (TAA), given in comparison with ThMA in the present invention
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                               ö
                                                                                                                                                             100.0%; Score 40; DB 4; Length 423; 100.0%; Pred. No. 17; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substitution; stability; activity; detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dishwashing agents; liquifaction agents
                                                                                                                                                                                                                                                                                                                                                 AAR46065 standard; protein; 478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Svendsen A, Bisgard-Frantzen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 7; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92DK-00000946.
92DK-00001503.
93DK-00000292.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                 137 SSQDYFH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-048855/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus oryzae
                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                1 SSQDYFH
                                                                                                                                Sequence 423 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-1992;
16-DEC-1992;
15-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9402597-A1
                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
18-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methionine
                                                                                                                                                                                                                                                                                                                                                                                  AAR46065;
                                                                                                                                                               Query Match
                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, bleaching and dyeing. The variants have improved thermostability, acid/alkaline stability, low temperature optimum; pH optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                  Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                  New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                 Thellersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                            Aspergillus oryzae alpha amylase (mature protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae alpha amylase (mature protein)
                                                                                                                                                                                                                                                                                                                                                                 Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 75-76; 105pp; English.
AAR72450 standard; protein; 478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR78270 standard; protein; 478 AA
                                                                                                                                                                                                                                                                                                                                                                 Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                      94WO-DK000370.
                                                                                                                                                                                                                                                                                              93DK-00001133.
94DK-00000140.
                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100
                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSQDYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-161790/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSODYFH 7
                                                                                                                                                                                        Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                 Borchert TV, |
Van Der Zee P;
                                                                                                                                                                thermostable.
                                                                                                                                                                                                                   WO9510603-A1
                                                                                                                                                                                                                                                                      05-OCT-1994;
                                                                                                                                                                                                                                                                                                 08-OCT-1993;
                                                                                                                                                                                                                                                                                                              02-FEB-1994;
                                                   25-MAR-2003
01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-1996
                                                                                                                                                                                                                                          20-APR-1995
                           AAR72450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR78270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
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Gaps

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Query Match 100.0%; Score 40; DB 2; Length 478; Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels

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/labels loop 1 modification region
/notes "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 8-18 of AAW14499 is deleted
or replaced with a fragment corresponding to this
fragment; claim 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28. 42
/label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13. .45
/label= loop 1 modification region
/label= loop 1 modification of residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 7-23 of AAW14499 is deleted or replaced with a
                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the mature form of taka-amylase from A. oryzae. This sequence was used in a method for the generation of mutant pullulanases for use in the food industry (see also AAR79026-28). The wild type pullulanase enzyme was modified by the method of the invention for enhancing the hydrophobicity of a selected site of the pullulanase. The method comprises replacement of a group in the selected site with a hydrophobic group, replacement of an amino acid with a hydrophobic anion acid, and/or insertion or deletion of a hydrophobic amino acid from the selected site. The method was used to produce neopullulanases Y377F,
                                                                                                                                                                                                                                                                              Modifying a transferase by enhancing hydrophobicity of a selected site increases transfer activity, also new mutant neo-pullulanase(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; eaclium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment corresponding to this fragment; claim 33'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 2; Length 478; 100.0%; Pred. No. 19; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oryzae alpha-amylase (mature protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sweetener; ethanol production; variant
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 10-11; 18pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW14500 standard; protein; 478
                                                         93JP-00306096
94JP-00288658
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                                                                                                                       (NIDE ) NEC CORP.
(EZAK ) EZAKI GLICO
                                                                                                                                                                                                                 WPI; 1995-279919/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus oryzae.
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Misc-difference اع
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S422V and M375L
31-OCT-1994;
                                                         12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1997
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Matches
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AAW14500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, sepecially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal origin can also be used. This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae,
   Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; amyloliquefaciens; Bacillus stearothermophilus; Aspergillus converses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of an oxidation stable alpha-amylase - for simultaneous desizing and bleaching or scouring of fabrics contg. starch or starch derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wild type; neopullulanase; B. stearothermophilus; mutant; food industry; modification; hydrophobicity; replacement insertion; deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nilsson TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pedersen HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR79025 standard; protein; 478 AA.
                                                                                                                                                                                                                                                                                                                                                                     94WO-DK000371.
                                                                                                                                                                                                                                                                                                                                                                                                                                  94DK-00000141
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Best Local Similarity luv...
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1 150, .164
1 240, .283
1 439, .474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toft AH, Marcher D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 SSODYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-283767/37
                                                                                                                                                                             Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus oryzae.
                                                                                                                Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSODYFH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond .
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                     05-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1994;
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                                                                                                                                                                                                                                                                                                        10-AUG-1995
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RESULT 5 AAR 79025

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Gaps

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a variant) corresponding to 325-345 of AAW14498 is deleted or replaced with a fragment corresponding to this fragment; claim 38"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-amylase variants and methods of production - have altered properties such as calcium dependency, substrate binding and stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is the mature Aspergillus oryzae alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alcohol; starch; dough improver; brewing; starch liquification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 40; DB 100.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                              Borchert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 87-88; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB84206 standard; protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                              Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                       96WO-DK000057.
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                                                                                                                                                                                                                                                   95DK-00000128
                                                                                                                                                                                                                                                                           95DK-00001192
95DK-00001256
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                                                                                                                                                                                                                                                                                                                                                NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 SSQDYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-371424/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSQDYFH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVOZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200134784-A1
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                                                                                                                                                                                                       05-FEB-1996;
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                                                                                                             WO9623874-A1
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                                                                                                                                                                                                                                                   03-FEB-1995;
23-OCT-1995;
                                                                                                                                                                                                                                                                                                 10-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                              Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2001
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/note= "at least one amino acid residue of a parent alpha
amylase (used as a template for a variant) corresponding
to 322-346 of AMV1498 is deleted or replaced with a
fragment corresponding to this fragment; claim 36"
                                                                                                        /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a templare for a variant) corresponding to 14-15 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                           //label= loop 2 modification region
//label= loop 2 modification acid residue of a parent alpha
//note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 44-57 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                      70. 78
//label= loop 2 modification region
//label= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 48-51 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98. .210
/label= loop 3 modification region
/label= loop 3 modification region
/note= wat least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "at least one amino acid residue of a parent alpha amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jabel= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
amylase (used as a template for a variant) corresponding
to 195-202 of AMM1499 is deleted or replaced with a
fragment corresponding to this fragment; claim 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166. 173
/label= loop 3 modification region
/label= loop 3 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 196-198 of AAW14499 is
deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= loop 8 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 121-181 of AAW14499 is
deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template fo a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-199 of AAWN14499; claim 42"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant
                                      fragment corresponding to this fragment; claim 30'
                   to 12-19 of AAW14499 is deleted or replaced with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= loop 3 modification region
                                                               32. .38
/label= loop 1 modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment; claim 23"
181. .184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fungamyl; claim 43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment; claim 26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 121. .174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                               Misc-difference
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specification describes variants of this fungamy1-like alpha-amylase, which have an alteration in one the amino acid regions 98-110, 150-160, 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion of substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic ph; relative to wild-type enzyme. The variants can therefore be used at higher temperatures (more efficient conversion or faster reaction, and have reduced need for cooling and reduced risk of contemination). The variants may also be used in conjunction with other enzymes, particularly glucoamylase during dextrinisation. The variants are used to produce syrups, particularly of high mallose content, or alcohol, from starch, as dough improver for baked goods; in brewing, to increase fermentability of the wort; and for liquefaction of starch
                                          variant of Fungamyl-like alpha-amylase, useful for production of tose syrups, includes mutations that improve stability against heat acidic pH.
                                                                                                                                                   present sequence represents a fungamyl-like alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 40; DB
100.0%; Pred. No. 20;
ive 0; Mismatches
                                                                                                                    Claim 1, Page 42-45; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADT89632 standard; protein; 498 AA.
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Matches 7; Conservative
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            WPI; 2001-367478/38.
N-PSDB; AAF90208.
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 498 AA;
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Gaps

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0; Indels

Aspergillus niger.

US2004191864-A1 30-SEP-2004 31-MAR-2004; 2004US-00815495.

(NOVO) NOVOZYMES BIOTECH INC

31-MAR-2003; 2003US-0459902P.

Connelly M, Brody H;

WPI; 2004-708545/69. N-PSDB; ADT89631.

Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological Bubstance

Example 11; SEQ ID NO 22; 58pp; English

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The present invention relates to a method of producing heterologous hological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance and second nucleotide heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequence comprising modification of glucosmylase (glash) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                             100.0%; Score 40; DB 8; Length 498 100.0%; Pred. No. 20;
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                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
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100.0%; Score 40; DB
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       ADT89628 standard; protein; 499 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                    SSODYFH 168
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N-PSDB; ADT89627.
                                                                                                                                                                                                                                                                  1 SSODYFH 7
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                                                                                                                                                             Sequence 498 AA;
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ADT89628
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Alpha-amylase, thermostable enzyme; baking, Aspergillus niger.

Thermomyces lanuginosus; CBS 224.63.

Location/Qualifiers 1. .18 /label= Sig_peptide

95WO-EP002607. 94GB-00013419.

03-JUL-1995; 04-JUL-1994;

WO9601323-A1

Peptide

18-JAN-1996

Michelsen B, Rasmussen P;

(DANI-) DANISCO AS.

WPI; 1996-087673/09.

N-PSDB; AAT10562

AAR88212 standard; protein; 493 AA.

AAR88212

(first entry)

Alpha-amylase

(revised)

16-OCT-2003 03-APR-1996

AAR88212;

SSODYFH 168

162

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The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose isomerase, or glucoamylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act processing enzymes, which are activated under suitable conditions to act plants and plant parts, e.g. grain, which express one or more of these enzymes and have an altered composition that facilitates plant and grain processing. Also described is a method (M) for converting starch to starch-derived products in a transformed plant part (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful or produce food products having improved taste and to produce fermentable substrates for channol and fermented beverages. (M) eliminates the need to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents alpha-amylase/glucoamylase fusion procein, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
                                                                                                                                                                                                                                                                                                                                                                           Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-qlucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme.
                                                                                                                                                                                                                                                                                                    Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craig J, Kinkema M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                           ABP96630 standard; protein; 1095 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 107; 158pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-2002; 2002WO-US027129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2001; 2001US-0315281P
                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus shirousami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-268420/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                      ABP96630
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RESULT 10
ABP96630
ABP96630
AAA ABP96630
AAA ABP96630
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Thermophilic alpha-amylase with activity range of 60-80 degrees C -derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs and bakery prods. esp. bread.

Claim 3; Page 36-38; 94pp; English.

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A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562) isolated from a T. lanuginosus gene library. The recombinant enzyme (54-60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7 and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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Pred. No. 76;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO08447 standard; protein; 52 AA.
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85.7%;
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Best Local Similarity
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Gaps

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Local Similarity 100.

Matches

141 SSQDYFH 147

RESULT 11

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16-JUL-1999;
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16-JUN-1
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1-NUL-80
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                                                                                                                                                                                                                                                                                                                             03-JUN
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                                                                                                                                                                                                                    The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to eryctokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides and polymerides are useful in gene therapy, vaccines or populations. The polymerides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, mematopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                     Claim 20; SEQ ID NO 22339; 1399pp + Sequence Listing; English.
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85.7%; Pred. No. 28;
iive 0; Mismatches 1; Indels
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99US-0123180P.
99US-0123548P.
99US-0125788P.
                                                                                                                      Tang YT, Liu C, Drmanac RT;
                                                26-FEB-2001; 2001WO-US004927
                                                                  28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2000 (first entry)
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                                                                                                                                        WPI; 2001-514838/56.
N-PSDB; AAI88378.
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                                                                                                 (HYSE-) HYSEQ INC
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         WO200164835-A2
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05-MAR-1999;
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Best Local S
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Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                         Score 34; DB 3; I
Pred. No. 7.5e+02;
0; Mismatches I,
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99US-0158232P
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Best Local Similarity
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26-OCT-1999;
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| 29  | 1160        | 43.2 | 200   | œ | ADS23436   | Ads23436 | Bacterial   |
| 30  | 1085        | 40.4 | 549   | ø | ABP97895   | Abp97895 | Amino aci   |
| 31  | 1015.5      | 37.8 | 513   | 8 | ADN19570   | Adn19570 | Bacterial   |
| 32  | 898.5       | 33.5 | 564   | æ | ADS44249   | Ad844249 | Bacterial   |
| 33  | 873         | 32.5 | 493   | œ | ADS44293   | Ads44293 | Bacteria    |
| 34  | 541         | 20.2 | 502   | 9 | ABU03092   | Abu03092 | Alpha amy   |
| 35  | 483.5       | 18.0 | 547   | œ | ADS30907   | Ad830907 | Bacteria    |
| 36  | 480.5       | 17.9 | 547   | œ | ADS30029   | Ad830029 | Bacteria]   |
| 37  | 456.5       | 17.0 | 713   | 7 | ADC23483   | Adc23483 | Bacillus    |
| 38  | 453         | 16.9 | 719,  | 4 | AAB74220   | Aab74220 | Bacillus    |
| 39  | 452.5       | 16.9 | 712   | ~ | AAR10051   | Aar10051 | Cyclomalt   |
| 40  | 452         | 16.8 | 719   | 4 | AAB74219   | Aab74219 | Bacillus    |
| 41  | 450         | 16.8 | 719   | ~ | AAY31731   | Aay31731 | Bacillus    |
| 42  | 450         | 16.8 | 719   | ~ | AAY30621   | Aay30621 | Amino act   |
| 43  | 450         | 16.8 | 719   | m | AAY94271   | Aay94271 | Bacillus    |
| 44- | 450         | 16.8 | 719   | 4 | AAB59956   | Aab59956 | Bacillus    |
| ٦,  | 450         | 16.8 | 719   | 4 | AAB74216   | Aab74216 | Bacillus    |

84444444

## ALIGNMENTS

Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose; alcohol; starch; dough improver; brewing; starch liquification. Amino acid sequence of a fungamyl-like alpha-amylase. Pedersen S; AAB84206 standard; protein; 498 AA Svendsen A, 10-NOV-2000; 2000WO-DK000626. 99DK-00001617 (first entry) (NOVO ) NOVOZYMES AS Bisgard-Frantzen H, Aspergillus oryzae WO200134784-A1 10-NOV-1999; 06-AUG-2001 17-MAY-2001 ABB4206

WPI; 2001-367478/38. N-PSDB; AAF90208.

New variant of Fungamyl-like alpha-amylase, useful for production of maltose syrups, includes mutations that improve stability against heat and acidic pH.

Claim 1; Page 42-45; 49pp; English.

The present sequence represents a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, which have an alteration in one the amino acid regions 98-110, 150-160, 161-167, 280-288, 484-455, and 468-457. Each alteration is a deletion or substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at a cidic pH, relative to wild-type enzyme. The variants can therefore be used at higher reduced need for cooling and reduced risk of contamination). The variants may also be used in conjunction with other enzymes, particularly glucoamylase during dextrinisation. The variants are used to produce

Alpha-amy

Variant Variant Variant Variant

AAR63185 AAR63187 AAR63186

51.8 51.7 49.9

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Glucoamylase; glaA; amyA; alpha-amylase A; enzyme
 Example 10; SEQ ID NO 18; 58pp; English
 Z
 498
 498
 499
 RVLYPTEKLAGSKICSSS
 standard; protein;
 entry)
WPI; 2004-708545/69.
N-PSDB; ADT89627.
 Sequence 499 AA;
 16-DEC-2004
 substance
 Query Match
Best Local S
Matches 496
 ~
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 62
 121
 241
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 301
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 482
 ADT89632
 ADT89632;
 481
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 360
 420
 420
 480
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 dough improver for baked goods; in brewing, to increase fermentability the wort; and for liquefaction of starch
or alcohol, from starch;
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
 VEDCKLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 MVAWWSIFLYGLOVAAPALAATPADWRSOSIYFLLTDRFARTDGSTTATCNTADOKYCGG
 TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 SDCPDSTILLCTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCF1QNYEDQTQ
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 Gaps
 ;
0
 498;
 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTA
 Aspergillus niger neutral alpha-amylase B (amyB) protein.
 Length
 Indels
 4;
 ö
 100.0%; Score 2684; DB 4
100.0%; Pred. No. 3e-226;
ive 0; Mismatches 0
syrups, particularly of high maltose content,
 Glucoamylase; glaA; amyB; alpha-amylase B;
 Ź
 RVLYPTEKLAGSKICSSS 498
 ADT89628 standard; protein; 499
 (NOVO) NOVOZYMES BIOTECH INC.
 31-MAR-2003; 2003US-0459902P.
 31-MAR-2004; 2004US-00815495
 (first entry)
 Best Local Similarity 100.
Matches 498; Conservative
 Brody
 Local Similarity
 Aspergillus niger
 Sequence 498 AA;
 US2004191864-A1
 Connelly M,
 30-SEP-2004
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 481
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 Query Match
 ADT89628
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The present invention relates to a method of producing heterologous halological substance. The method involves culturing mutant of wild-type hapergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance and second nucleotide heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.
 300
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
 301
 SDCPDSTLLGTPVENHDNPRFASYTNDIALAKAVAAFIILNDGIPIIYAGQEQHYAGGND 361
 481
Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDXSVFRPFSSODYFHPFCFLONYEDOTO
 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 PANREATWLSGYPTDSELYKLIASRNAIRNYAISKOTGFVTYKAWPIYKODTTIPMRKGT
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 MVAWWSLFLYGLQVAAPALAATPADWRSQS1YFLLTDRFARTDGSTTATCNTADQKYCGG
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 Gaps
 ö
 tch al Similarity 99.6%; Score 2674; DB 8; Length 499; al Similarity 99.6%; Pred. No. 2.38-225; 496; Conservative 0; Mismatches 2; Indels
 Aspergillus niger neutral alpha-amylase A (amyA) protein
```

240

241

181

360

420

421

480

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9 61 120

121

Mon

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WPI; 1995-161790/21.
 Aspergillus oryzae.
 Sequence 478 AA;
 Van Der Zee P;
 thermostable.
 05-OCT-1994;
 WO9510603-A1
 Borchert IV,
 25-MAR-2003
01-DEC-1995
 20-APR-1995
 AAR72450;
 21
 81
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 201
 181
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 The present invention relates to a method of producing heterologous halological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequence comprising medification of glucosmylase (glash) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
 240
 Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
 120
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWFGYN 241
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEbQTQ 180
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT 420
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 480
 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 121
 301
 361
 421
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 481
 9
 19
 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAGNVAAFIILNDGIPIIYAGQEQHYAGGND
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQODIYSLNENYGTADDL
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 PANREATWLSGYPTDSELYKLIASRNAIRNYAISKDTGFVTYKOWPIYKODTTIPMRKGT
 Gaps
 ;
0
 Length 498;
 2; Indels
 Score 2662; DB 8;
Pred. No. 2.6e-224;
0; Mismatches 2;
 Example 11; SEQ ID NO 22; 58pp; English.
 (NOVO) NOVOZYMES BIOTECH INC
 99.2%;
 31-MAR-2004; 2004US-00815495
 31-MAR-2003; 2003US-0459902P
 481 RVLYPTEKLAGSKIC 495
 Matches 493; Conservative
 Connelly M, Brody H;
 WPI; 2004-708545/69
 Best Local Similarity
 Aspergillus niger.
 N-PSDB; ADT89631
 Sequence 498 AA;
 JS2004191864-A1
 30-SEP-2004
 substance.
 122
 241
 242
 61
 121
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 Query Match
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Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, blacching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-WAR-2003 to correct PN field.)
 ö
 260
 140
 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 200
 NHWGYDGAGSSVDYSVFKPFSSGDYFHPPCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180
 240
 80
 9
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGXNKAAGVYCIGEVLDGDPAYTC
 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
 Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
 New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance.
 ó
 Thellersen M;
 Length 478;
 Indele
 Aspergillus oryzae alpha amylase (mature protein).
 Score 2572; DB 2;
Pred. No. 1.9e-216;
0; Mismatches 1;
 Svendsen A,
 New Bacillus derived alpha-amylase variants
 Disclosure, Page 75-76, 105pp, English.
 Ź
 Bisgard-Frantzen H,
 AAR72450 standard; protein; 478
 93DK-00001133.
94DK-00000140.
 94WO-DK000370
 95.8%;
99.8%;
 (revised)
(first entry)
 Query Match
Best Local Similarity 99.8
Matches 477; Conservative
482 RVLYPTEKLAGSKIC
 (NOVO) NOVO-NORDISK AS.
```

180

260

200

140

240

320

478

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LIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 LIASANAIRNYAISKDTGFVTYKOWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 PYQNVMDGVLNYP1YYPLLNAFKSTSGSMDDLYNM1NTVKSDCPDSTLLGTFVENHDNPR
 AAW14500 standard, protein;
 Aspergillus oryzae.
 Key
Misc-difference
 Misc-difference
 Misc-difference
 04-JUN-1997
 241
81
 121
 181
 361
 441
 421
 AAW14500;
 141
 201
 321
 381
 261
 RESULT 6
AAW14500
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 Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal origin can also be used. This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae
 300
 FASYTNDIALAKNVAAFIILNDGIPIIYAGGEQHYAGGNDPANREATWLSGYPTDSELYK 360
 LIASANAIRNYAISKDIGFVTYKNWPIYKDDITIIAMRKGIDGSQIVTILSNKCASGDSYT 440
 420
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 and
 Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus;
 LSLSGAGYTAGOQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 Use of an oxidation stable alpha-amylase - for simultaneous desizing bleaching or scouring of fabrics contg. starch or starch derivs.
 Length 478;
 Aspergillus oryzae alpha amylase (mature protein)
 Score 2572; DB 2;
Pred. No. 1.9e-216;
0; Mismatches 1;
 Nilsson
 Disclosure; Page 25-26; 37pp; English.
 Pedersen HH,
 Æ
 AAR78270 standard; protein; 478
 94WO-DK000371.
 94DK-00000141
 Match 95.8%;
Local Similarity 99.8%;
les 477; Conservative
 (first entry)
 (NOVO) NOVO-NORDISK AS
 Toft AH, Marcher D,
 WPI; 1995-283767/37.
 Aspergillus oryzae.
 Aspergillus oryzae
 Sequence 478 AA
 05-OCT-1994;
 02-FEB-1994;
 W09521247-A1
 10-AUG-1995.
 241
 301
 AAR78270;
 261
 321
 381
 361
 441
 421
 Query Match
 AARTASTO
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32. .38
/label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
 28. .42
/label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 12.19 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 30"
 13. .45
/label= loop 1 modification region
/label= loop 1 modification region
/note= wat least one amino acid residue of a parent alpha
-amylage (used as a template for a variant) corresponding
to 7-23 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 33"
 for
 14. .40
/label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template fo
a variant) corresponding to 8-18 of AAW14499 is deleted
or replaced with a fragment corresponding to this
fragment; claim 35"
 alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; acalcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction;
 Aspergillus oryzae alpha-amylase (mature protein).
 sweetener; ethanol production; variant
 Location/Qualifiers
(first entry)
 Misc-difference
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Gaps

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Indels

80 9

ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI ATPADWRSQSIVFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI

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Best Loca Matches

methods of production - have altered dependency, substrate binding and stability.

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Borchert

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The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl- and fungamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cysteine residues in the variant is modified or replaced with a non-proline or non-cystein residue such as alanine. The variants can be used for (dish) washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of sweeteners and ethanol from starch. See also AAM14498-99
 Disclosure; Page 87-88; 171pp; English
 Bisgard-Frantzen
 95DK-00000128.
95DK-00001192.
95DK-00001256.
 96WO-DK000057
 Alpha-amylase variants and
 properties such as calcium
 NOVO) NOVO-NORDISK AS
 WPI; 1996-371424/37
 Sequence 478 AA;
 23-OCT-1995;
10-NOV-1995;
 05-FEB-1996;
 J3-FEB-1995;
 Svendsen A,
 08-AUG-1996
 321
 301
 361
 441
 81
 141
 261
 381
 Query Match
 201
 421
 Matches
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 8
 /label= loop 2 modification region
/note= "at least one amino acid residue of a parent alpha
amylase (used as a template for a variant) corresponding
to 44-57 of AAM14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
 98. .210
/label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
 /label= loop 3 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 121-181 of AAW14499 is
deleted or replaced with a fragment corresponding to this
fragment; claim 26"
 165. 177
/label= loop 3 modification region
/label= loop 3 modification acid residue of a parent alpha
-loop a template for a variant) corresponding
to 195-202 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 21"
 /label= loop 3 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 196-198 of AAW14499 is
deleted or replaced with a fragment corresponding to this
fragment; claim 23"
 for
 for
 for
 /note= "at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
 to this
aeleted
 deleted
 or
 to this
a variant
 /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template f a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-199 of AAW14499; claim 42"
 /_note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template fa variant) corresponding to 325-345 of AAW14498 is deleted or replaced with a fragment corresponding to the fragment; claim 38"
 /label= loop 2 modification region
/label= loop 2 modification region
residue of a parent alpha-amylase (used as a template
a variant) corresponding to 48-51 of AAW14499 is delete
or replaced with a fragment corresponding to this
 corresponding to this fragment; claim 24"
 corresponding to this fragment; claim 36
 or replaced with a fragment corresponding to this
 to 14-15 of AAW14499 is
 /note= "an amino acid fragment corresponding tregion is deleted from the parent sequence of Fungamyl; claim 43"
 297. .313
/label= loop 8 modification region
 corresponding
 fragment; claim 32"
 66. .84
/label= loop 2
 variant)
 .181
 fragment
 fragment
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
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 Misc-difference
 Misc-difference
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180
 140
 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 200
 260
 240
 320
 420
 241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 LIASANAIRNYAISKDIGFVIYKNWPIYKDDITIAMRKGIDGSQIVTILSNKGASGDSYT 440
 80
 9
 478
 498
 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 181 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
 LSESGAGYTAGOOLTEVIGCTTVTVGSDGNVPVPMAGGEPRVLYPTEKLAGSKICSSS
 ;
0
 Length 478;
 Indels
 Score 2572; DB 2;
Pred. No. 1.9e-216;
 0; Mismatches
 ABP96630 standard; protein; 1095
95.8%;
Local Similarity 99.8%;
Res 477; Conservative (
 RESULT 7
ABP96630
ID ABP9
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WO9623874-A1

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conzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose isomerase, or glucoamylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are asophilic, thermophilic or hyperthermophilic processing enzymes, which are solidable conditions to act upon the desired substrate. Also described are self-processing transgenic plants and plant parts, e.g. grain, which express one or more of these plants and plant parte of composition that facilitates plant and grain processing. Also described is a method (M) for converting starch to starch processing enzyme contained in it. Transgenic grain is useful for preparing maltodextrin. A transformed plant (TPP), by activating for preparing maltodextrin, A transformed plant (TP) can be used to produce food products having improved taste and to produce fermentable substrates for ethanol and fermented beverages. (M) eliminates the need to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents
 Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
 180
 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
 201 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
 80
 9
 present invention describes polynucleotides which encode processing
 Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme.
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
 Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
 ö
 Kinkema M;
 Length 1095;
 Indele
 Craig J,
 ï
 95.7%; Score 2569; DB 6; 99.8%; Pred. No. 1.3e-215; iive 0; Mismatches 1;
 Chen W,
 exemplification of the present invention
 (SYGN) SYNGENTA PARTICIPATIONS AG.
 Claim 1; Page 107; 158pp; English.
 Batie CJ,
 27-AUG-2002; 2002WO-US027129.
 27-AUG-2001; 2001US-0315281P
 (first entry)
 Query Match
Best Local Similarity 99.8
Matches 477; Conservative
 Aspergillus shirousami
 Lanahan MB, Basu SS,
 2003-268420/26.
 Sequence 1095 AA;
 WPI; 2003-268420/
N-PSDB; ACC44572.
 WO2003018766-A2
 06-MAR-2003.
 Synthetic.
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ABP96630;
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 Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
 The sequence os that of the Asoergillus oryzae alpha amylase, sold commercially as FUNCAMYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PN field.)
 300
 440
FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 421 LSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
 PYQNVMDGVLNYP1YYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 LIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT
 Gaps
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
 ;
0
 95.1%; Score 2552; DB 2; Length 478; 99.4%; Pred. No. 1.1e-214; ive 0; Mismatches 3; Indels (
 Methionine substitution, stability, activity, detergent, dishwashing agents, liquifaction agents.
 AAR46065 standard; protein; 478 AA
 Bisgard-Frantzen H;
 Claim 1; Page 7; 20pp; English.
 92DK-00000946.
92DK-00001503.
93DK-00000292.
 93WO-DK000230.
 (revised)
(first entry)
 Query Match
Best Local Similarity 99.4
Matches 475; Conservative
 (NOVO) NOVO-NORDISK AS.
 Mutant alpha-amylase.
 WPI; 1994-048855/06.
 Aspergillus oryzae.
 Sequence 478 AA;
 WO9402597-A1.
 06-JUL-1993;
 23-JUL-1992;
 15-MAR-1993;
 Svendsen A,
 25-MAR-2003
18-JUL-1994
 03-FEB-1994.
 AAR46065;
 241
 321
 381
 441
 AAR46065
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241 PYQNVMDGVLNYPIXYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 301 FASYINDIALAKAVAAFIILNDGLPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
This sequence represents the mature form of taka-amylase from A. oryzae. This sequence was used in a method for the generation of mutant pullulanases for use in the food industry (see also ARR79026-28). The wild type pullulanase enzyme was modified by the method of the invention for enhancing the hydrophobicity of a selected site of the pullulanase. The method comprises replacement of a group in the selected site with a hydrophobic group, replacement of an amino acid with a hydrophobic amino acid, and/or insertion or deletion of a hydrophobic amino acid selected site. The method was used to produce neopullulanases Y377F, selected site.
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation; protein co-ordinate data; 3 dimensional structure.
 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
 61 WITPVTAQLPQDCAYGDAYTGYWQTDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
 361 LIASANAIRNYAISKDIGFVIYKN-PYIKDDITIAMRKGIDGSQIVTILSNKGASGDSYT
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 LIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 1;
 2; Length 478;
 Indels
 .
.
 Match 93.3%; Score 2503.5; DB Local Similarity 97.9%; Pred. No. 2e-210; les 468; Conservative 1; Mismatches 8
 oryzae TAKA protein (TAA)
 Z
 423
 99KR-00039130
 99KR-00039130
 ABB09072 standard; protein;
 (first entry)
 Aspergillus oryzae.
 Sequence 478 AA
 19-SEP-1999;
 09-SEP-1999;
 Aspergillus
 26-JUN-2002
 06-APR-2001
 Query Match
Best Local S:
Matches 468
 321
 441
 141
 201
 261
 381
 RESULT 1
 886666666668888
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 200
 260
 240
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 440
 FASYTNDIALAKOVVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 9
 Wild type; neopullulanase; B. stearothermophilus; mutant; food industry; modification; hydrophobicity; replacement insertion; deletion.
 LSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPVPWAGGLPRVLYPTEKLAGSKICSSS 498
 a transferase by enhancing hydrophobicity of a selected site transfer activity, also new mutant neo-pullulanase(s).
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 LIASANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYT
 ATPADWRSQSIYFLIDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Disclosure; Page 10-11; 18pp; English
 Location/Qualifiers
 Ş
 AAR79025 standard; protein; 478
 94JP-00288658
 30. .38
150. .164
240. .283
439. .474
 22-MAR-1996 (first entry)
 ŝ
 Mature taka-amylase A.
 WPI; 1995-279919/37.
 (NIDE) NEC CORP.
(EZAK) EZAKI GLICO
 Aspergillus oryzae
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 JP07177891-A.
 31-OCT-1994;
 12-NOV-1993;
 18-JUL-1995
 Modifying increases
 121
 19
 181
 241
 21
 81
 141
 201
 321
 301
 361
 261
 421
 AAR79025;
 381
 441
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260 240 320 440 419

477

140 120 200

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The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic amylase. Manufacturing maltogenic amylase comprises the following steps: (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 50278) and inserting the gene into plasmid put119 to construct recombinant DNA (prhMA118); (ii) inserting the recombinant DNA to Escherichia coli M11061, which is cultivated at 37 plus degrees Celius for 10 hours in Luria-Bertani (LB) media and centrifuging the media to obtain a microbial cell; (iii) suspending the microbial cell with buffer solution at pH 7.5 and obtaining supernatant; and (iv) passing the supernatant through column chromatography and obtaining purified maltogenic amylase. The maltogenic amylase is a dimer comprised of two maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase (ThMA) crystal The amylase has a structure containing an activated region that consists of amino acid residues of Asp-328 (du-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of Pro44, Tyr45, Arg81, Arg81, Asm181, Glu1312, Val1329, and Hisl360. The present sequence represents Appergillus oryzae TAKA protein (TAA), given in comparison with ThMA in the present invention
 Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
 Disclosure; Page 188; 196pp; Korean.
(POST-) POSTECH FOUND.
(SAMY-) SAMYANG GENEX CORP.
 WPI; 2001-534477/59
 Park GH;
 Kim TJ,
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Sequence 423 AA;

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384
 444
 144
 61 VIAQLPQTTAYGDAMHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDMVANHMG 120
 145 YDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVK 204
 240
 324
 300
 TNDIALAKNVAAFIILNDGMPKIYWGQEQHYAGGNDPANREATWLSGYPTDSELYKLIAS 360
 361 ANAIRNYAISKDIGEVTYKOWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLS 420
 205 NEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQN 264
 84
 9
 1 DWRSQSIYFLLIDRFARIDGSITATGNTADQKYGGGTWQCIIDKLDYIQGMGFTAIWITP
 NEWYDWVGSLVSNYSIDGERIDIVKHVDKDFWRQYNXAAGVYQIGEVLDGDPAYTCPYQN
 VMDGVLNYP1YYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASY
 VMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRRASY
 TNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIAS
 85 VTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMG
 ANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLS
 DWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITP
 Gaps
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Query Match 80.1%; Score 2151; DB 4; Length 423; Best Local Similarity 95.7%; Pred. No. 1.4e-179; Matches 405; Conservative 2; Mismatches 16; Indels
 GAG 447
 GAG 423
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RESULT 11

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ABB80177 standard; protein; 495 AA.
ABB80177
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(first entry) 11-AUG-2003

A. fumigatus AfAAL1

Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase; beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability.

Aspergillus fumigatus.

WO2003012071-A2.

13-FEB-2003

05-AUG-2002; 2002WO-US024842.

03-AUG-2001; 2001US-0309870P.

(ELIT-) ELITRA PHARM INC.

Bussey H; Roemer T, Jiang B, Storms R,

WPI; 2003-332729/31

N-PSDB; ABQ80345, ABQ80346.

Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.

Claim 17; Page 134-35; 169pp; English.

to composition. Compositions comprising beta-galactosidases are useful for modulating the amount of lactose in a composition. Compositions comprising beta-galactosidases are useful for modulating the amount of sucrose in a composition. Composition of sucrose in a composition. Composition of sucrose in a composition. Composition of sucrose in a composition. Composition of sucrose in a composition. Composition of starches or maltodextring in a composition. Composition of oxidated phenolic carcase are useful for modulating the amount of oxidated phenolic composition. Composition. Compositions comprising polygalacturonases are useful for modulating the amount of oxidated phenolic composition. The amount of thigh or low molecular weight composition and composition or sylo-oligomers or are useful for modulating the amount of xylan or xylo-oligomers or are useful for modulating the amount of xylan or xylo-oligomers or a composition. The A. funigatus proteins and corresponding pha, a are useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to compare with the nucleocide sequence of A. funigatus confidential uses, to compare with the nucleocide sequence of A. funigatus confidential activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify operated or distant fungal organisms to identify operated or distant fungal organisms to identify operated or distant fungal organism to identify of attachment to a nucleic acid array for examination of expression The sequences given in ABB80164-87 show enzymatic proteins derived from A. fumigatus. These proteins display the catalytic activity of an enzyme such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, betagalactosidases, invertaes, lipase, alpha-amylase, laccase, polygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of compounds that comprise a gallate ester linkage in a composition. Compositions comprising cellulase are useful for modulating the amount of cellulose in a composition composition amount of glucose or oxygen in a composition composition to amount of glucose or oxygen in a composition comprising phytase are useful for modulating the amount of myo-inosition comprising phytase are useful for modulating the amount of myo-inosition phosphates

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16-AUG-2001; 2001EP-00000382.
16-AUG-2001; 2001EP-00000383.
16-AUG-2001; 2001EP-00000384.
 Sequence 494 AA;
 (STAM) DSM NV
 present
 11-AUG-2003
 Query Match
Best Local Si
Matches 364;
 246
 485
 Ď,
 186
 306
 365
 482
 ABB80178
 ABB80178;
 Maier
 RESULT 13
ABB80178
ID ABB8
XX
AC ABB8
XX
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XX
DT 11-A
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 180
 121
 120
 181
 241
 240
 301
 360
 420
 300
 361
 421
 GSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPR 481
 61
 9
patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour. Havour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions
 QCADSTLLGTFVENHDTPRFASYTKDWALAKNAAAFIIFSDGIPIIYAGGEGHYSGGADP
 WOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLK
 ALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQV
 EDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNK
 VAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGT
 AAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKS
 DCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDP
 ANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTD
 Gaps
 Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosidic linkage; oligosaccharide; polysaccharide; baking.
 5
 sequence of an alpha-amylase of Aspergillus niger
 495;
 Indels
 78.2%; Score 2100; DB 6; Length 78.6%; Pred. No. 5.3e-175; ive 39; Mismatches 65; Indels
 Æ.
 494
 16-AUG-2001; 2001EP-00000379.
16-AUG-2001; 2001EP-00000380.
16-AUG-2001; 2001EP-00000381.
 VLYPTEKLAGSKICS 496
 | ||| | || :|:
VFYPTAGLNGSTVCT 495
 02-AUG-2002; 2002WO-NL000522
 standard; protein;
 Query Match
Best Local Similarity 78.64
Matches 389, Conservative
 (first entry)
 Aspergillus niger
 Š
 WO2003016535-A2
 17-JUN-2003
 27-FEB-2003
 acid
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 Sequence
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 filamentous fungus
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 65
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 Aspergillus niger. Alpha-amylases catalyse the endohydrolysis of 1,4-alpha-apluosidid: linkages in oligosaccharides and polysaccharides. The alpha-amylase polymucleorides and polypeptides of the invention are useful in a baking process
 242 YCIGEVFDGDASYTCPYQEDLDGVLNYPMYYPLERAFESTNGSISDLYNMINTVKSTCRD
 302 STLLGTFVENHDNPRFAKSYTSDMSLAKNAATFTILADGIPIIYAGQEQHYSGGNDPYNR
 2 TIFLFLAIFVATALAATPAEWRSQSIYFLLTDRFARTDNSTTASCDLSARQYCGGSWQGI
 66 IDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSS
 126 ALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCW
 LGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGV
 YCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPD
 362 BATWLSGYKTTSELYTHIAASNKIRTHAIKQDTGYLTYKNYPIYQDTSTLAMRKGYNGTO
 6 SLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGI
 STLLGTFVENHDNPRFA-SYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANR
 EATWLSGYPIDSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQ
 425 IVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLY
 Gaps
 fungus, preferably Aspergillus
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 ..
 Length 494;
 Indels
 sequence is an alpha-amylase enzyme of the
 Albermann
 65;
 DB 6;
 75.0%; Score 2012; DB 6; 73.8%; Pred. No. 2.8e-167; ive 62; Mismatches 65
 Ď,
 Folkers
 New polynucleotide from a filamentous
niger, useful in a baking process.
 Claim 13; Page 61-63; 81pp; English
 Ą.
 630
 ပဲ
 protein;
Wagner
 496
 494
 Local Similarity 73.8
es 364; Conservative
 PTEKLA-GSKICS
 PADKLVNGSSFCS
 WPI, 2003-312758/30
 (first
 A. fumigatus AfAAL2
Stock A,
 standard;
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beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain, xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability. tannase; cellulase; glucose oxidase; glucoamylase; phytase;

Aspergillus fumigatus.

WO2003012071-A2

13-FEB-2003.

05-AUG-2002; 2002WO-US024842.

03-AUG-2001; 2001US-0309870P

(ELIT-) ELITRA PHARM INC.

Bussey H; Roemer T, Jiang B, Storms R,

N-PSDB; ABQ80347, ABQ80348. 2003-332729/31

Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.

Claim 17; Page 139-40; 169pp; English

A. tunigatus. These processes display the caralytic activity of an enzyme cuch as tannase, cellulase, glucose oxidase, glucoamylase, phytase, betagated ucuch as tannase, cellulase, lipase, alpha-amylase, lacase, phytase, polygalacturonase or xylanase. Compositions comprise a gallate cupical for modulating the amount of collulose in a composition comprising callulase are useful for modulating the amount of cellulose in a composition comprising the amount of compositions comprising the amount of composition. Compositions comprising the amount of composition composition. Compositions comprising phytase are useful for modulating the amount of acceptance or oxygen in a composition. Compositions comprising phytase are useful for modulating the amount of lactose in a composition. Composition composition composition. Compositions comprising sucrase or invertase are useful for modulating the amount of glactose in a composition composition composition composition. Compositions comprising sucrase or invertase are useful for modulating the amount of glactose in a composition composition composition composition composition composition composition composition composition composition composition composition composition for modulating the amount of bidh or low molecular weight composition are useful for modulating the amount of high or low molecular weight polygalacturonic acid chains in a composition. Compositions comprising composition composition composition composition composition in various industries such as those involved in the making of food composition in various industries such as those involved in the making of food captores recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleoxide sequence of Alfundation or composition in various industries such as those involved in the making of captone of other related or distant fungal organisms to identify duplicated genes, for sequence of contextial orthologous enzyme genes, for sequence of characterial orthologous enzyme genes, sequences given in ABB80164-87 show enzymatic proteins derived from tumigatus. These proteins display the catalytic activity of an enzyme fumigatus.

Sequence 630 AA;

Felby C, Fuglsang CC;

Veit C,

WPI; 2002-479793/51

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7
 182
 359
 303 ASDCADPILIGNFIEWHDNPRFASYTSDXSQAKNVISFWFFSDGIPIVYAGQEQHYSGGA 362
 422
 478
 60 GTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADD 119
 63 GSWQGIINHLDYIQGMGFTAIWITPVTEQFYENTGDGTSYHGYWQQNIHEVNANYGTAQD 122
 179
 239
 299
 DPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKG 419
 62
 Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
 5 WSLFLYGLQVAAPAL----AATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCG
 3 WISQLFPLSLCSSLLGQAAHALTPAEWRSQSIYFLLTDRFGREDNSTTAACDVTQRLYCG
 183 AVEDCWLGDTTVSLPDLDTTSTAVRSIWYDWVKGLVANYSIDGLRIDTVKHVEKDFWPGY
 KSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGN
 T-DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGG
 LKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCF1QNYEDQT
 180 QVEDCWLGDNTVSLPDLDTTXDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQXDFWPGY
 NKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTV
 Gaps
 9
Length 630;
 Indels
 pred. No. 1.4e-151;
59; Mismatches 101;
 68.4%; Score 1835; DB 6;
66.8%; Pred. No. 1.4e-151;
 Aspergillus niger alpha-amylase protein.
 (NOVO) NOVOZYMES AS.
(NOVO) NOVOZYMES NORTH AMERICA INC.
 AAE24207 standard; protein; 484 AA
 LPRVLYPTEKLAGSKICSSS 498
 483 LPRVFVPSSWVSGSGLCGDS
 10-NOV-2000; 2000DK-00001676.
21-NOV-2000; 2000US-0252213P.
11-DEC-2000; 2000DK-00001854.
 09-NOV-2001; 2001WO-DK000737
 15-DEC-2000; 2000US-0256015P
 (first entry)
 334; Conservative
 Similarity
 Aspergillus niger.
 WO200238787-A2
 04-OCT-2002
 16-MAY-2002
 AAE24207;
 120
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The invention relates to a method for producing ethanol from starch-containing material, by fermentation. The method involves carrying out a secondary liquefaction step in the presence of a thermostable acid alpha-amylase. The method is used in producing ethanol from a starch-containing material such as tubers, roots or whole grain (e.g. corn, wheat or barley or their combination) or combination of the materials. Preferably ethanol is produced from starch-containing material that is obtained from cereals or from corns, cobs, wheat, barley, rye, milo and potatoes or their combination. The ethanol produced by above mentioned method is used as fuel alcohol and/or fuel additive. The ethanol is also useful as drinking ethanol i.e., potable neutral spirits or industrial ethanol. The present sequence is Aspergillus niger alpha-amylase protein
 Producing ethanol from starch-containing material e.g., tubers, roots, whole grain, for use in fuel, by fermentation comprises carrying out a secondary liquefaction step in the presence of a thermostable acid alpha-
 Claim 35; Page 31-33; 33pp; English.
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YTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIA 383 ASWRIQSIYFLLIDRFGRIDNSTTATCNIGNEIYCGGSWQGIIDHLDYIEGMGFTAIWIS PVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHM GYDGAGSSVDYSVFKPFSSQDYFHPPCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVV KNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQ NVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFAS ADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWIT 66.2%; Score 1778; DB 5; Length 484; 66.9%; Pred. No. 9.1e-147; ive 63; Mismatches 94; Indels ( Local Similarity 66.9 es 318; Conservative Sequence 484 AA; 24 84 64 Query Match 144 204 184 264 304 ઠે 요 ઠે 셤 ઠે 셤 ઠે g ð 요 ઠે 요

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enzyme; alcohol; slurry; water; granular starch; acid alpha-amylase;
glucoamylase; gelatinization; yeast; beer; fuel ethanol; potable ethanol;
industrial ethanol.
 Aspergillus niger acid alpha-amylase for ethanol production method
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 ADS75939 standard; protein;
 16-DEC-2004
 ADS75939
ADS75939
ID ADS7
XX AC ADS7
XX DT 16-D
XX XX BE
XX ASPE
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XX ASPE
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XX ASPE
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The invention relates to a method for the production of an alcohol product by holding a slurry of water and granular starch in the presence of an acid alpha-amylase and a glucoamylase at 0-20 deg C below the initial gelatinization temperature of the granular starch; holding the slurry in the presence of acid alpha-amylase, glucoamylase and yeast at 10-35 deg C to produce ethanol; and optionally recovering the ethanol. The method is used for the production of an alcohol product such as beer or recovered ethanol, e.g. fuel ethanol, potable ethanol or industrial ethanol. This sequence represents an acid fungal alpha-amylase from Aspergillus niger used in the method of the invention.
 Production of alcohol product, e.g. beer, comprises holding slurry of water and granular starch in presence of acid alpha-amylase and glucoamylase followed by simultaneous saccharification and fermentation.
 Festersen RM
 9; SEQ ID NO 1; 43pp; English,
 10-MAR-2003; 2003US-0453326P.
 ŝ
 WPI; 2004-677503/66
 (NOVO) NOVOZYMES
 Sequence 484 AA;
 WO2004080923-A2
 23-SEP-2004
 Olsen HS,
 Claim
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ö Gaps ö Indels 94; 66.2%; Score 1778; DB 8; 66.9%; Pred. No. 9.1e-147; 63; Mismatches Query Match
Best Local Similarity 66.9
Matches 318; Conservative

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SGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS

SANAIRNYAISKOTGFVTYKOWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYTLSL

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143
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 263
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 244 KVLDGVLNYPIYWQLLYAFESSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPRFAK 303
 383
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 123
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 264 NVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFAS 323
 83
 63
 24 ADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWIT
 84 PVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHM
 GYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVV
 204 KNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQ
 324 YINDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIA
 384 SANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSL
 144
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364 TIWAIRKLAIAADSAYITYANDAFYIDSWIIAMAKGISGSQVIIVLSNKGSSGSSYTLTL 478 498 SGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 444 셤

Search completed: February 8, 2005, 18:36:39 Job time : 293.866 secs

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 Sequence 7, A
Sequence 7, A
Sequence 7, A
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 Sequence 72,
Sequence 28,
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-08-720-899-7
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US-08-600-9084-10
US-09-182-859-7
US-09-182-859-7
US-09-182-859-7
US-09-636-252A-10
US-09-636-252A-10
US-08-470-702-6
US-08-470-702-6
US-08-470-702-7
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 Total number of hits satisfying chosen parameters:
 513545 segs, 74649064 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Issued Patents AA:*
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-10-820-200-2
2684
 Query
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 Title:
Perfect score:
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 Seguence:
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| US-08-484-434C-35<br>US-09-384-361.35<br>US-08-469-202-27<br>US-08-484-434C-34<br>US-08-347-365-2<br>US-08-947-965-7<br>US-08-947-965-71<br>US-08-947-965-71<br>US-08-947-965-71<br>US-08-947-965-72<br>US-08-947-965-74<br>US-08-947-965-74<br>US-08-947-965-74<br>US-08-947-965-74<br>US-08-947-965-74<br>US-08-947-965-74<br>US-08-947-965-74                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ALIGNMENTS Henrik edel ne ARIANTS 5753460disk of No. e, 64th Floor 100, Version #1.30 20,899 41.0, Version #1.30                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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| 655<br>655<br>655<br>655<br>668<br>676<br>686<br>683<br>1938<br>1938<br>685<br>685<br>685<br>685<br>685<br>685<br>685<br>685<br>685<br>68                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | On                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | A Application US/08720899 1. 5753460 1. 1NFORMATION: ANNT: Biggaard-Frantzen, H ANNT: Biggaard-Frantzen, H ANNT: Biggaard-Frantzen, H ANNT: Thellersen, Marianne ANNT: Thellersen, Marianne ANNT: Thellersen, Marianne ANNT: Van der Zee, Pia OF INWENTION: ANYLASE VAR OF INWENTION: ANYLASE VAR 1 OF SEQUENCES: 38 18 NOW YORK ESSEE: No. 57534600 No. 5 18 New York ESSEE: No. 57534600 No. 5 18 New York ESSEE: No. 57534600 No. 5 11 ON TYPE: ISB COMPADABLE FORM: UNT TYPE: ISB COMPADABLE FORM: 10174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401 110174-6401  |
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Length 478, Indels

Query Match 95.8%; Score 2572; DB 1; Best Local Similarity 99.8%; Pred. No. 3.2e-220; Matches 477; Conservative 0; Mismatches 1;

LENGTH: 478 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-720-899-7

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LENGTH: 478 amino acids TYPE: amino acid
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US-08-459-610-7
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 Sequence 7, Application US/08459610

Sequence 7, Application US/08459610

Sequence 7, Application US/08459610

Sequence 7, Application US/08459610

SEXERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
STARET: A05 Lexington Avenue, 64th Floor
CITY: New York
 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 61 WITPVTAQLEQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMYDVVA 120
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 COUNTRY. USA

ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-UWN 1995
CLASSIFICATION: 435
 NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOWNUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
 RESULT 2
US-08-459-610-7
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US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Thellersen, Marianne
APPLICANT: Thellersen, Marianne
APPLICANT: Wan der Zee, Pia
; TTILE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58308370 No. 5830837th America, Inc.
STREET: New York
CITY: New York
STATE: New York
COUNTRY: USA
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 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180
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 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
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 Length 478
 1; Indels
 COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 95.8%; Score 2572; DB 1;
99.8%; Pred. No. 3.2e-220;
iive 0; Mismatches 1;
 APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
FILING SITECATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
 Query Match
Best Local Similarity 99.8 Matches 477; Conservative
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-600-908A-10
 201
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 Query Match
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 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
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 Sequence 10, Application US/08600908A
Patent No. 5989169
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Brorchert, Torben Vedel
TITLE OF INVENTION: -Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 59891690 No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
 9
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
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 Gaps
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 Length 478;
 1; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 Query Match
95.8%; Score 2572; DB 2;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1;
 CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDENNESS: single
 ; TOPOLOGY: linear
US-08-343-804-7
 RESULT 4
US-08-600-908A-10
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 ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
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 ;
0
 Length 478;
 95.8%; Score 2572; DB 2;
99.8%; Pred. No. 3.2e-220;
tive 0; Mismatches 1;
 STREET: 405 Lexington Avenue, 64th Floor CITY: New York
 US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Bornert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/600,908A FILING DATE: 13-FEB-1996
 STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
 FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 anino acids
TYPE: amino acid
 Best Local Similarity 99.8 Matches 477; Conservative
 single
 MOLECULE TYPE: CDNA
 STRANDEDNESS: Bir
TOPOLOGY: linear
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FILE REFERENCE: 4796.204-US
CURRENT APPLICATION UNDHER: US/09/182,859
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-07-12
EARLIER PILING DATE: 1996-07-11
EARLIER PILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 7
SEQ ID NO 7
TITLE OF INVENTION: Alpha-Amylase Mutants
 ; Sequence 7, Application US/09672459; Patent No. 6436888
 ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7
 Query Match 95.8
Best Local Similarity 99.8
Matches 477; Conservative
 US-09-672-459-7
 181
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 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGWYLMVDVVA 120
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 Gaps
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 Length 478
 1; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 Score 2572; DB 3;
Pred. No. 3.2e-220;
0; Mismatches 1;
 FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
 Sequence 7, Application US/09182859; Patent No. 6143708; GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
 95.8%;
 SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
 Query Match 95.8
Best Local Similarity 99.8
Matches 477; Conservative
 STRANDEDNESS: single
TOPOLOGY: linear
COMPUTER READABLE FORM:
 TOPOLOGY: linear MOLECULE TYPE: CDNA
 US-08-683-838A-10
 US-09-182-859-7
 201
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DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 240
 PYQNVMDGVLNYPIYYPLLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
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 361 LIASANAIRNYAISKDTGFVTYKNWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT 420
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 Length 478
 1; Indels
95.8%; Score 2572; DB 3; 99.8%; Pred. No. 3.2e-220; ive 0; Mismatches 1;
 GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERRNCE: 4796-204-08
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1999-10-29
FRIOR FILING DATE: 1999-10-29
FRIOR FILING DATE: 1999-10-29
FRIOR FILING DATE: 1999-10-29
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FASYTUDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 301 FASYINDIALAKAVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 LIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
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 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEXLAGSKICSSS 498
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 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
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 Length 478
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 Length
 Query Match 95.8%; Score 2572; DB 4;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1;
 Query Match 95.8%; Score 2572; DB 4; Best Local Similarity 99.8%; Pred. No. 3.2e-220; Matches 477; Conservative 0; Mismatches 1;
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Blesgard-Frantzen, Henrik
FILE REFERENCE: 4796,204-US
CURRENT APPLICATION WUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR PRILING DATE: 1000-09-28
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-38
PRIOR FILING DATE: 1996-01-1
PRIOR FILING DATE: 1996-01-1
SEQ ID NOS: 37
SEQ ID NO 7
SEQ ID NO 7
 Sequence 7, Application US/10186042; Patent No. 6642044; GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
 US-10-186-042-7
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 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
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 301 PASYTNDIALAKAVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 LIASANAIRNYAISKOTGEVTYKANPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 361 LIASANAIRNYAISKOTGFVTYKAWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT 420
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
 441 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSBS 498
 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
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 Length 478;
 1; Indels
 95.8%; Score 2572; DB 4;
99.8%; Pred. No. 3.2e-220;
tive 0; Mismatches 1;
 Sequence 10, Application US/09636252A

Sequence 10, Application US/09636252A

Patent No. 6440716

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert. Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT PILING DATE: 2000-08-10
PRIOR PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR PLING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
 ; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7
 Matches 477; Conservative
 Query Match
Best Local Similarity
 t TYPE: PRTORGANISM: A. oryzaeUS-09-636-252A-10
 US-09-636-252A-10
 141
 201
 181
 261
 241
 321
 381
 SEQ ID NO 7
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PYONYMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
 241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 301 FASYINDIALAKAVAAFIILNDGLPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 LIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 61 WITPVTAQLPQDCAYGDAYTGYWQTDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 APPLICANT: MATSUT, IKUO
APPLICANT: ISHIKWA, KAZUHIKO
APPLICANT: ISHIKWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MIYAIRI, SACHIO
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: B110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
 441 LSLSGAGYTAGQOLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKTAGSKICSSS 498
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 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
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 Score 2503.5; DB 2; Length 478; Pred. No. 4e-214; 1; Mismatches 8; Indels 1;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 6, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
TELEFAX: ZUE
TELEFAX: ZUE
TELEFX: ZUES16
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
"UDE: amino acids
"UDE: amino acid
 Query Match 93.3%;
Best Local Similarity 97.9%;
Matches 468; Conservative 1
 TOPOLOGY: linear; MOLECULE TYPE: protein US-08-339-715A-2
 22042
 US-08-470-702-6
 81
 141
 181
 321
 381
 420
 201
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 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180
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 240
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
 241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 FASYTNDIALAKNVAAFIILANGIPIIXAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
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 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takada, Toshikazu
APPLICANT: Takada, Toshikazu
APPLICANT: Shimada, Jiro
APPLICANT: Shimada, Jiro
APPLICANT: Yanase, Michiyo
APPLICANT: Yanase, Michiyo
APPLICANT: Takata, Michiyo
APPLICANT: Takata, Michiyo
APPLICANT: Takata, Michiyo
APPLICANT: Takata, Michiyo
APPLICANT: Takata, Michiyo
APPLICANT: Takata, Michiyo
APPLICANT: Okada, Shigetaka
APPLICANT: Okada, Angeraka
APPLICANT: Okada, Hark, Schobrican APPLICANT:
APPLICANT: POPHAW, HAIK, SCHNOBRICH & KAUFMAN, LTD.
STREET: G. Street
CITY: Washington
STRATE: D.C.
COUNTRY: USA
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
CORPUTER: IEM PC compatible
CORPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,715A
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
PRICASSIFICATION DATA:
APPLICATION NUMBER: US/08/393
FILING DATE: 12-NOV-1993
ATORNEY AGENT INFORMATION:
NAME: Melser, Allen S
REFERENCE/DOCKET NUMBER: 18335.009
TELECOMMUNICATION INFORMATION:
 US-08-339-715A-2; Sequence 2, Application US/08339715A; Patent No. 5965442...
 ZIP: 20005
 181
 81
 141
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 261
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 421
 21
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PELICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTOMNER: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERNICE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (703) 205-8000
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEX: 248345
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
 (703) 205-8050
 259; Conservative
TITLE OF INVENTION: VAR
TITLE OF INVENTION: VAR
TITLE OF INVENTION: OLINUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 single
 linear
 amino acid
 Similarity
 STRANDEDNESS:
 22042
 TELEFAX:
 US-08-467-831-6
 Query Match
Best Local :
 Best Loca
Matches
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 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
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 22 TPAD-WRSQSIYFLLTDRFFARTDGSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI
 441 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS 496
 Gaps
 10;
 Length 468;
 Query Match
51.9%; Score 1392; DB 1; Length 4(
Best Local Similarity 54.4%; Pred. No. 3.1e-115;
Matches 259; Conservative 81; Mismatches 126; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-WAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
 Sequence 6, Application US/08467831
Patent No. 5815378
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: HONDA, KOICHI
APPLICANT: HONDA, KOICHI
 LENGTH: 468 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 ANTI-SENSE: NO
 RESULT 12
US-08-467-831-6
 US-08-470-702-6
 261
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62 WISPVVENIPDNTAYGYAYHGFWMKNIYKINENFGTADDLKSLAQELHDRDMLLMVDIVT 121
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VARIANT-TYPE CARBOHYDRATE HYDROLASE, VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING OLIGOSACCHARIDE USING THE ENZYME
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 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 51.9%; Score 1392; DB 1;
54.4%; Pred. No. 3.1e-115;
tive 81; Mismatches 126;
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church STATE: Virginia COUNTRY: U.S.A.
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TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
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 Indels
 ; Score 1391; DB 1; I
; Pred. No. 3.8e-115;
81; Mismatches 126;
 Patentin Release #1.0, Version #1.25
 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatchouse Road, Suite 500 East
 SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702 FILING DATE: 06-UN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656 FILING DATE: 02-MAR-1994 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 7, Application US/08470702 Patent No. 5631149
 NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFRENCE/DOCKET NUMBER: 234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
 APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
 51.8%;
 LENGTH: 468 amino acids
 Query Match
Best Local Similarity 54.4[†]
Matches 259† Conservative
 TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
 amino acid
 linear
 GENERAL INFORMATION:
 STRANDEDNESS:
 RESULT 14
US-08-470-702-7
 US-08-470-702-7
 321
 381
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 APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant -Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET UNMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 205-8050
TELEFAX: (703) 205-8050
 LLP
 51.8%; Score 1391; DB 1; 54.4%; Pred. No. 3.8e-115; tive 81; Mismatches 126;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch,
STREET: 8110 Gatehouse Road, Suite 500 East
 Sequence 4, Application US/08204656B Patent No. 5538882
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INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 468 amino acids
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 Query Match
Best Local Similarity 54.4
Matches 259; Conservative
 , MOLECULE TYPE: protein US-08-204-656B-4
 CITY: Falls Church
STATE: Virginia
 linear
 COUNTRY: U.S.A.
 GENERAL INFORMATION:
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Search completed: February
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 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
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 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: MINZAITI, STEMA
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
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 417 VIISNIGYSSGEDLVEVLICSTVSGSSD--LQVSIQGGQQQIFVPAK--YASDICS
 CUNTRY: Virginia
COUNTRY: U.S.A.

ZIF: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATIONEY/AGENT INFORMATION:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church
 NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
 Sequence 7, Application US/08467831
Patent No. 5635378
GENERAL INFORMATION:
 (703) 205-8000
(703) 205-8050
 TELEX: 248345
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein;
HYPOTHETICAL: NO
ANTI-SENSE: NO
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## ALIGNMENTS

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Sequence 18, Application US/10815495
; Publication No. US20040191864A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brody, Howard
ITILE OF INVENTION: Mathems of Aspergillus Niger
TITLE OF INVENTION: Mutants Of Aspergillus Niger
TITLE OF INVENTION: Mutants Of Aspergillus Niger
TITLE OF INVENTION: Mutants Of Aspergillus Niger
TITLE OF INVENTION: Mutants Of Aspergillus Niger
CURRENT APPLICATION WUMBER: US/10/815,495
CURRENT APPLICATION WUMBER: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 499
TYPE: PRT

CREANISM: Aspergillus niger
US-10-815-495-18
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Pred. No. 1.6e-212;
0; Mismatches 2;
 Query Match
Best Local Similarity 99.6%;
Matches 496; Conservative
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PUBLICACION NO. US20030170769A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 1996-07-18
PRIOR FILING DATE: 1996-07-18
SPRIOR FILING DATE: 1996-07-18
SOFTWARE: FREESE FOR MINGOWS Version 3.0
SEQ ID NO 10
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nes 477; Conservative
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; ORGANISM: A. Oryzae
US-10-184-771-10
 US-10-184-771-10
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 Query Match
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 Sequence 22, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
APPLICANT: Brody, Howard
APPLICANT: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REFERENCE: 10345.200-US
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 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIXYPLLNAFKSTSGSMDDLYNMINTVK 301
 9
 61
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYS1DGLR1DTVKHVQKDFWPGYN
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 Gaps
 ô
 Score 2662; DB 16; Length 498;
Pred. No. 1.6e-211;
0; Mismatches 2; Indels 0
 CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 22
LENGTH: 498
 RVLYPTEKLAGSKICSSS 498
 Query Match
Best Local Similarity 99.6%;
Matches 493; Conservative
 ; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22
 RESULT 2
US-10-815-495-22
 242
 362
 121
 302
 241
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 61
 181
 241
 242
 181
 361
 481
 301
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LENGTH: 478
 US-10-644-187-7
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 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 61 WITPVTAQLEQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMYDVVA 120
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPPCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
 121 NHMGYDGAGSSVDXSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCMLGDNTVSLPDLDTTK 180
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
 DVVKNEWYDHVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 240
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
 241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 LIASANAIRNYAISKOTGFVTYKNWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT 420
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS6S 478
 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
 ö
 Length 478;
 Indels
 Query Match 95.8%; Score 2572; DB 14; Best Local Similarity 99.8%; Pred. No. 4.1e-204; Matches 477; Conservative 0; Mismatches 1;
 Sequence 7, Application US/10186042

Publication No. US200301712361

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-011
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-11-08
PRIOR FILING DATE: 1996-11-08
SEQ ID NO 7:
SEQ ID NO 7:
SEQ ID NO 7:
SEQ ID NO 7:
SEQ ID NO 7:
 ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
 181
 381
 141
 201
 261
 361
 441
 421
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RESULT

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 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180
 260
 240
 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
 241 PYQNVMDGVLNYPIYYPLLANFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 361 LIASANAIRNYAISKOTGFVTYKOWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT 420
 89
 9
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
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 Length 478;
 IndelB
 Score 2572; DB 15;
Pred. No. 4.1e-204;
 95.8%; Scor.
99.8%; Pred. No. 4...
 APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
TITLE REFERENCE: 4796, 204-US
CURRENT APPLICATION NUMBER: US/10/644,187
CURRENT FILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRALESEQ for Windows Version 3.0
 RESULL v
US-10-26-720-10
Sequence 10, Application US/10926720
Sequence 10, Application No. US20050019886Al
Publication No. US20050019886Al
GENERAL INPORMATION:
APPLICANT: Svendsen, Allan
Bisg+rd-Frantzen, Henrik
Sequence 7, Application US/10644187
Publication No. USZO040048351A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
 TYPE: PRT ORGANISM: Bacillus licheniformis
 Query Match
Best Local Similarity 99.8
Matches 477; Conservative
```

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Sequence 42, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
GENERAL INFORMATION:
BUSSEY, HOWARD
APPLICANT: Jiang, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
 200
 180
 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 260
 241 PYQNVMDGVLNYPIXYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 361 LIASANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYT 420
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 LSLSGAGYTAGOQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 421 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPPCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 PYQNVMDGVLNYP1 YYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
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 95.7%; Score 2569; DB 14; Length 1095; 99.8%; Pred. No. 2.3e-203; ive 0; Mismatches 1; Indels 0;
 US-10-228-061-45

Sequence 45, Application US/10228063

Sequence 45, Application US/10228063

Publication No. US20030135885A1

GENERAL INFORMATION:

APPLICANT: Lanahan, Mike

TITLE OF INVENTION: Self-processing Plants and Plant Parts

FILE REFERENCE: 10946.317

CURRENT APPLICATION NUMBER: US/10/228,063

CURRENT FILING DATE: 2002-12-12

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 45
 LENGTH: 1095
TYPE: PRT
ORGANISM: Aspergillus shirousami
 Best Local Similarity 99.8 Matches 477; Conservative
 RESULT 8
US-10-213-990-42
 US-10-228-063-45
 441
 201
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 Query Match
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 320
 61 WITPVTAGLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
 180
 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 301 FASYTNDIALAKOVVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
 LIASANAIRNYAISKOTGFVTYKWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT 420
 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
 80
 9
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 PYQNVMDGVLNYP1XYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDXLDYIQGMGFTAI
 Gaps
 ö
 Query Match 95.8%; Score 2572; DB 17; Length 478; Best Local Similarity 99.8%; Pred. No. 4.1e-204; Matches 477; Conservative 0; Mismatches 1; Indels 0
 COUNTYER READABLE STATES OF AMERICA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: 1BM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/926,720
FILING DATE: 26-Aug-2004
CLASSIFICATION: -UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 38,475
TELEPHONE: 212-867-0123
 ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York STATE: New York
 TITLE OF INVENTION: -Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
 TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO: 10:
 TYPE: amino acid
STRANDEDNESS: single
 SEQUENCE CHARACTERISTICS
 MOLECULE
 241
 81
 141
 121
 181
 261
 361
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 321
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299
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 242
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 302
 300 KSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGN 359
 303 ASDCADPILLGNFIEWHDNPRPASYTSDYSQAKNVISFWFFSDGIPIVVAGQEQHYSGGA 362
 143
 62
 83
 63
 63 GSWQGIINHLDYIQGMGFTAIWIITPVTEQFYENTGDGTSYHGYWQQNIHEVNANYGTAQD
 3 WISQLFPLSLCSSLLGQAAHALTPAEWRSQSIYFLLTDRFGREDNSTTAACDVTQRLYCG
 240 NKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTV
 243 NDAAGVYCVGEVPSGDPQYTCPYQNYLDGVLNYPIYYQLLYAFQSTSGSISNLYNMISSV
 360 DPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKG
 4 ASWRIQSIYFLLIDRFGRIDNSTIATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWIS
 ----AATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCG
 60 GTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADD
 120 LKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQT
 123 LRDLANALHARGMYLAVDVVANHAGYNGAGNSVNYGVFTPFDSATYFHPYCLITDYNNQT
 180 QVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGY
 183 AVEDCWLGDTTVSLPDLDTTSTAVRSIWYDWVKGLVANYSIDGLRIDTVKHVEKDFWPGY
 420 T-DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGG
 24 ADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWIT
 84 PVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHM
 Gapa
 °,
 Sequence 1, Application US/10416393
Publication No. US20040091983A1
Publication No. US20040091983A1
Publication No. US20040091983A1
APPLICANT: Veit, Cristopher
APPLICANT: Felby, Claus
APPLICANT: Fugleang, Claus
TITLE OF INVENTION: SECONDARY LIQUEFACTION IN ETHANOL PRODUCTION
FILE REPERENCE: 10113.204-US
CURRENT APPLICATION NUMBER: US/10/416,393
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.2
 Length 484;
 Indels
 Query Match 66.2%; Score 1778; DB 15; Best Local Similarity 66.9%; Pred. No. 2.2e-138; Matches 318; Conservative 63; Mismatches 94;
 479 LPRVLYPTEKLAGSKICSSS 498
 483 LPRVFVPSSWVSGSGLCGDS 502
 FEATURE:
NAMEKKEY: misc feature
OTHER INERMATION: SEQ ID NO:1
US-10-416-393-1
 ORGANISM: Aspergillus niger
 WSLFLYGLQVAAPAL-
 LENGTH: 484
TYPE: PRT
 US-10-416-393-1
 SEQ ID NO 1
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 APPLICANT: Jiang, Bo.
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
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 AAGVYCIGEVFDGDPAYTCPYQEVLDGVLNYPIXYPLLKAFQSTSGSMSSLYDMINTVKS 300
 360
 421 GAQIITVLSNLGASGSSYTLSLGGGGGGEAGOOLTEMFSCTTVTVGSDKKVPVSMASGLPR 480
 61 WQGIIEQLDXIQGMGFTAIMITPVTKQLPQDTSEGTAYHGYWQQDIYSVNSNYGTADDLK 120
 EDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNK 241
 ANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTD 421
 GSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPR 481
 WQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLK 121
 122 ALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQV 181
 AAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKS 301
 DCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDP 361
 9
 3 IRWSSFFLSCL--AGTALAATPAQWRSQSIYFLLTDRFARTDGSTTASCDTSAREYCGGT
 301 QCADSTLLGTFVENHDTPRFASYTKDMALAKNAAAFIIFSDGIPIIYAGQEQHYSGGADP
 2 VAWWSLFLYGLOVAAPALAATPADWRSOSIYFLLTDRFARTDGSTTATCNTADOKYCGGT
 Gaps
 Gaps
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 9
 Length 495;
 Length 630;
 Query Match 78.2%; Score 2100; DB 14; Length Best Local Similarity 78.6%; Pred. No. 5e-165; Matches 389; Conservative 39; Mismatches 65; Indels
 Indels
 68.4%; Score 1835; DB 14;
66.8%; Pred. No. 6e-143;
iive 59; Mismatches 101;
for Windows Version 4.0
 Sequence 45, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
 VLYPTEKLAGSKICS 496
 481 VFYPTAGLNGSTVCT 495
 Matches 334, Conservative
 ; ORGANISM: Aspergillus
US-10-213-990-42
 ORGANISM: Aspergillus
 Best Local Similarity
 SOFTWARE: FastSEQ
SEQ ID NO 42
 US-10-213-990-45
 US-10-213-990-45
 LENGTH: 495
 302
 62
 182
 241
 362
 482
 181
 242
 361
 422
 Query Match
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us-10-820-200-2.rapb

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 480
 486
 ENHDLPRFASLKODINVSRLKPSASPIRLNNFSLAKNILTFTLLFDGLPIIYQGQEQHFS 360
 GGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTG-FVTYKNWPIYKDDTTIA 415
 MRKGTDGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPM 475
 79 AIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDV 138
 243 SVDIICGYQSNIMPSVTNYPIYFALLDAF--TIGDTESLPNQVESMKSKCPSVTSLTIFS 300
308 QTCSDVTALISFSENHDVARFASFKDDIALAKNVLIFIMLFDGIPMIYQGQEQHFSGASD 367
 139 VANHMGYDGAGSS----VDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLP 194
 DLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDG 254
 ENHDNPRFASYTNDI -------ALAKNVAAFIILNDGIPIIYAGQEQHYA 356
 62
 PANREATWLSGYPTDSELYKLIASANAIRNYALSKDTGFVTYKOWPIYKDDTTIAMRKGT
 DPAYTCPYQ-NVMDGVLNYPIXYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFV
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 19 LAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFT
 Gaps
 56;
 Length 500;
 43.2%; Score 1160; DB 15; Length 44.8%; Pred. No. 3.2e-87; ive 83; Mismatches 167; Indels
 ; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-12469
 |||:| : : || :|
RVLFPADMMEGSGLC 501
 RVLYPTEKLAGSKIC 495
 Matches 224; Conservative
 Similarity
 368
 428
 63
 183
 255
 301
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 Sequence 48 Application US/10213990
| Sequence 48 Application US/2030082595A1
| Sevence 48 Application No. US20030082595A1
| GENERAL INFORMATION:
| APPLICANT: Ususey, Howard
| APPLICANT: Roemer, Terry
| APPLICANT: Roemer, Terry
| TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
| TITLE OF INVENTION: NUCLEIC ACIDS OF USE
| FILE REFERENCE: 10182-019-999
| CURRENT APPLICATION NUMBER: US/10/213,990
| CURRENT PILING DATE: 2002-08-05
| NUMBER OF SEQ ID NOS: 72
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 48
| LENGTH: 547
 263
 NVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFAS 323
 443
 423
 124
 129
 240
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKAVAAFIILNDGIPIIYAGGEQHYAGGND 360
GYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVV 203
 YTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIA 383
 SALHERGMYLMVDVVANHMGY--DG--AGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
 64
 69
 65 IIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALS
 KNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQ
 SANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYTLSL
 WSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQG
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 Gaps
 498
 SGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
 DB 14; Length 547;
 .,
 Query Match
45.2%; Score 1214.5; DB 14; Lengt
Best Local Similarity 46.5%; Pred. No. 1.1e-91;
Matches 230; Conservative 79; Mismatches 179; Indels
 ; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-48
 124
 184
 264
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 304
 384
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
 78 TAIWITPVTAQLP-QTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMV 136
 198 DLDVESSDVSSYLSDHFKSLISKYDFDGLRIDAVKAMYTFFPDFVDATGVYSVGEVFSY 257
 312
 258 DPDTMCSYMSVLPGVTNYFLQLYINFSFTATGAGFTLIPTYQEVMASNCSKYDSTLMLTF 317
 378 DOSNPYYTVIKTMVAPRKRVITQDPDMVT-----STYQSIESAVDHYVGQKNDVLV 428
 137 DVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFI--QNYEDQTQVEDCWLGDNTVSLP 194
 195 DLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDG 254
 373 PTDSELYKLIASANAIRNYAISKDTGFVTYKOWPIYKDDTTIAMRKGTD-----GSQIVT 427
 428 ILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTE 487
 78
 18 ALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGF
 DPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCP--DSTLLGTF
 313 VENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGY
 33.5%; Score 898.5; DB 15; Length 564; 38.8%; Pred. No. 1.6e-65; Live 85; Mismatches 190; Indels 21;
 US-10-369-493-22723, Application US/10369493; Sequence 22723, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION: APPLICANT: Cao, Yongweir; APPLICANT: Hinkle, Gregory J. APPLICANT: Hinkle, Gregory C.; APPLICANT: Goldman, Barry S.
 Sequence 22679, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
 ORGANISM: Schizosaccharomyces pombe
 Matches 188; Conservative
 NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22679
 Best Local Similarity
 488 KLAG 491
 KMSG 491
 US-10-369-493-22679
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 APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 47374
 298 -NLVAHHCKDSTLLGLFLESQDAPRLAALANDYTVLKNAMTLNLMSDGIPIVFYGQEQMF 356
 66 GIIDKLDYIQGMGFTAIWISPIIKNIEGRTXYGEAYHGYWPQDLYTLNPHFGTEQDLIDL 125
 244 GVYCQGEEWIGQADLFCEWQEYMDGLHNFPVQGVAAESVIPLNDRALRKTAIAM---- 297
 FRKGREGRQIIMVLSTQGSNSGAYTIRMMN-GFQPSVVARDVFSCRTWTVNDMGELFLDM 479
 GIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKAL 123
 SSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVED 183
 CWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAA 243
 244 GVYCIGEVLDGDPAYTCPYQNVMDGVLNYPI-----YYPLLN-AFKSTSGSMDDLYNM 295
 296 INTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHY 355
 414 IAMRKGTDGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNV-P 472
 356 AGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTG--FVTYKWWPIYKDDTT 413
 5 WSL-FLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQ 63
 Gaps
 Query Match 37.8%; Score 1015.5; DB 15; Length 513; Best Local Similarity 41.4%; Pred. No. 3e-75; Matches 204; Conservative 84; Mismatches 170; Indels 35;
 ; Sequence 2223, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
 ORGANISM: Schizosaccharomyces pombe
 476 AGGLPRVLYPTEKLAGSKIC 495
 OKGEPRVLFPEALMRGSGLC 499
 473 VPMAGGLPRVLYP 485
 : | |::|||
TSIKKGEPKILYP 478
 10-369-493-2223
 US-10-369-493-2223
 SEQ ID NO 2223
LENGTH: 513
 64
 124
 184
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 RESULT
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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR RILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SEQ ID NO 2: 47374
SEQ ID NO 2:723
LENGTH: 493
 86 TAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMGY 145
 146 DGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKN 205
 EWYDWYGSLVSNYSIDGLRIDTVKHYQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQNV 265
 196 FFQNWVSDLIKRYQFDGIRLDTAKHVEKSFFPTFIEAANVFTTGEVFHGDPKVVGDYQKY 255
 316 TKDIAVSLLNNISIXYLHFLYILTFIXLALNALTALIFMDGIPIIYYGQEQMFDGGSDPD 375
 363 NREATWISGYPIDSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKDDTT-IAMRKGID 421
 422 GSQIVTILSNKGA-SGDSYTLSLSGAGYTAGQQLTBVIGCTTVTVGSDGNVPVPMAGGLP 480
 266 MDGVLNYPIYYPLLNAFKSTSGSMDDLYN-MINTVKSDCPDSTLLGTFVENHDNPRFASY 324
 325 TNDIA-------LAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPA 362
 16
 26 WRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITPV 85
 19 WRKQVIYQVLTDRFALDEDNFYA--KASGNLYLGGTWKGITRNLDYIKSLGCTAIWISPI
 Gaps
 Query Match 32.5%; Score 873; DB 15; Length 493; Best Local Similarity 37.8%; Pred. No. 1.7e-63; Matches 182; Conservative 84; Mismatches 182; Indels 34;
 FEATURE:

NAME/KEY: unsure

LOCATION: (1)...(493)

COTATION: UNSURE at all Xaa locations
US-10-369-493-22723
 rch completed: February 8, 2005, 19:05:52 time : 223.723 secs
 TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February

8, 2005, 18:28:34; Search time 57.6834 Seconds (without alignments) 830.671 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-820-200-2 2684 1 MVAWWSLFLYGLQVAAPALA......LPRVLYPTEKLAGSKICSSS 498

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | •                     |         |               |               |        |        |               |               |        |        |        |               |               |               |               |        |               |               |          |                |               |                    |               |              |               |                   |                   |                   |                   |               |
|-----------|-----------------------|---------|---------------|---------------|--------|--------|---------------|---------------|--------|--------|--------|---------------|---------------|---------------|---------------|--------|---------------|---------------|----------|----------------|---------------|--------------------|---------------|--------------|---------------|-------------------|-------------------|-------------------|-------------------|---------------|
|           |                       | (EC     | )<br>일        | (BC           | (EC    | (BC    | (BC           | _             | (BC    | (BC    | (EC 3. | (BC           | OE)           | (BC           | (EC           | (EC    | a pr          | - #           | -amy     | -amy           | - 5           | -amy               | EC<br>(EC     | (EC 3        | homod         | rin               | rin               | rin               | rin               | EC            |
|           | uo                    | lase    | lase          | lase          | lase   | lase   | alpha-amylase | alpha-amylase | lase   | lase   | Be (E  | labe          | labe          | lase          | lase          | lase   | lase          | lase          | alpha    | probable alpha | lase          | probable alpha-amy | lase          | аве (        | lase          | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | lase          |
|           | Description           | amylase | alpha-amylase | alpha-amylase | ı-amy  | ı-amy  | ı-amy         | ı-amy         | ı-amy  | 1-amy  | ılana  | alpha-amylabe | alpha-amylabe | alpha-amylase | alpha-amylase | t-amy  | alpha-amylase | alpha-amylase | ple      | ble            | alpha-amylase | ple                | alpha-amylase | beta-атујаве | alpha-amylase | malt.             | malt.             | malt              | malt              | alpha-amylase |
|           | Desci                 | alpha-  | alphe         | alpha         | alpha  | alpha  | alphe         | alpha         | alphe  | alpha  | pull r | alpha         | alpha         | alpha         | alphe         | alpha  | alpha         | alphe         | probable | probe          | alpha         | proba              | alphe         | beta-        | alphe         | cyclo             | cyclo             | cyclc             | cycle             | alpha         |
|           |                       |         |               |               |        |        |               |               |        |        |        |               |               |               |               |        |               |               |          |                |               |                    |               |              |               |                   |                   |                   |                   |               |
|           |                       |         |               |               |        |        |               |               |        |        |        |               |               |               |               |        |               |               |          |                |               |                    |               |              |               |                   |                   |                   |                   |               |
|           |                       |         |               |               |        |        |               |               |        |        |        |               |               |               |               |        |               |               |          |                |               |                    |               |              |               |                   |                   |                   |                   |               |
| RIES      |                       |         |               |               |        |        |               |               |        |        |        |               |               |               |               |        |               |               |          |                |               |                    |               |              |               |                   |                   |                   |                   |               |
| SUMMARIES |                       | S1      | 663           | 83            | 305    | 588    | 305           | 466           | 201    | 282    | 510    | 921           | 115           | 355           | YAF           | 270    | 770           | 603           | 448      | 505            | 503           | 860                | 478           | 130          | 539           | 827               | SG1               | SG3               | SG7               | SK            |
| -         | Ð                     | ALAS1   | JS0663        | ALAS3         | B48305 | JN0588 | A48305        | JT0466        | JK0201 | A35282 | JC4510 | 533921        | 806115        | 823355        | ALBYAF        | 872270 | T38770        | T41           | T38448   | 862505         | T41503        | T40                | 531478        | A29130       | T39539        | AI1827            | ALBSG1            | ALBSG3            | ALBSG7            | ALBSK         |
|           | 80                    | п       | 7             | ч             | N      | N      | 7             | ~             | 7      | Н      | ٦      | ~             | N             | ~             | Н             | ~      | ~             | 0             | ~        | ~              | ~             | ~                  | ~             | 7            | N             | 0                 | н                 | Н                 | Н                 | Н             |
|           | Query<br>Match Length | 499     | 499           | 499           | 499    | 499    | 498           | 499           | 478    | 484    | 624    | 507           | 512           | 512           | 494           | 631    | 513           | 625           | 491      | 581            | 564           | 478                | 482           | 1196         | 774           | 642               | 713               | 712               | 713               | 528           |
|           | 상인                    | 0       | .7            | 9.66          | 9.     | 9.     | ~             | 0.            |        | ۳.     |        | 56.9          | 0             | 53.9          | =             | ۲.     | 8.            | 6             | <u>ج</u> | 'n.            | .5            | 5.                 | ō.            | 0            | ლ:            | 6.                | 7.0               | ٥.                | 9                 | 4.            |
| d         | Query                 | 100.0   | 56            | 6             | 6      | 6      | 6             | 66            | 93     | 99     | 9      | 56            | 54            | 53            | 22            | 47     | 37            | 35            | 34       | 33             | 33            | 33                 | 27            | 25           | 24            | 17                | 17                | 16                | 16                | 16            |
|           | Score                 | 2684    | 2675          | 2674          | 674    | 673    | 2662          | 2656          | 3.5    | 780    | 629    | 527           | 449           | 1445.5        | 7.5           | 264    | 5.5           | 963.5         | 0.5      | 899            | 8.5           | 868                | 737           | 670          | 3.5           | 1.5               | •                 | 4.5               | 4.5               | 40.5          |
|           | လွ                    | 7       | 7             | ~             | 7      | 7      | ~             | 7             | 250    | ٦      | ٦      | Н             | ٦             | 144           | 139           | ٦      | 101           | 96            | 92       |                | 8             |                    |               |              | 65            | 48                | 45                | 454               | 44                | 44            |
|           | Result<br>No.         |         | N             | m             | 4      | 3      | 9             | 7             | 80     | 0      | 10     | 11            | 12            | 13            | 14            | 15     | 16            | 17            | 18       | 19             | 20            | 21                 | 22            | 23           | 24            | 25                | 26                |                   |                   | 29            |

| cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | alpha-amylase (EC | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | alpha-amylase (EC | glycosyl hydrolase | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | cyclomaltodextrin | alpha-amylase (EC |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| 863598            | ALKBG             | ALBSX1            | 828179            | A58800 '          | ALBSGR            | 809196            | S28784            | G75392             | 139805            | ALBSGC            | ALBSG6            | ALBSXR            | ALBSMX            | ALBSXF            | A60999            |
| ~                 | н                 | ч                 | ~                 | ~                 | ч                 | N                 | н                 | N                  | N                 | н                 | Н                 | ٦                 | ٦                 | 7                 | 7                 |
| 710               | 655               | 703               | 919               | 713               | 714               | 713               | 717               | 483                | 704               | 718               | 718               | 713               | 718               | 711               | 1104              |
| 16.1              | 16.0              | 15.9              | 15.8              | 15.6              | 15.6              | 15.4              | 15.4              | 15.3               | 15.2              | 15.1              | 15.1              | 15.1              | 14.9              | 14.3              | 14.0              |
| 433               | 428.5             | 428               | 424.5             | 418               | 418               | 414.5             | 412               | 410                | 407               | 406.5             | 405.5             | 405               | 399.5             | 384.5             | 376.5             |
| 30                | 31                | 32                | 33                | 34                | 32                | 36                | 37                | 38                 | 39                | 40                | 41                | 42                | 43                | 44                | 45                |

## ALIGNMENTS

| RESULT 1 ALAS1 Alabel 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                     |
|-------------------------------------------------------------------------------------------------------------------------------------------------|
| alpha-amylase (b. 3.2.1.1) I precured; [valuated] - Abrergillus olyzae NyAlternate names; alpha-amylase isozyme II; glycogenase; Taka-amylase A |
| C;Species: Aspergillus oryzae<br>C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2                                       |
| C;Accession: S04548; A33214; JS0240; A91930; A93767; A10627<br>p.wires1                                                                         |
| Mol. Microbiol. 3, 3-14, 1989                                                                                                                   |
| A, Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identic                                                                       |
| A; Reference number: S04548; MUID:89237897; PMID:2785629                                                                                        |
| A; Accession: S04548                                                                                                                            |
| A; Molecule type: DNA                                                                                                                           |
| A. Besidines: 1-400 vwtb.                                                                                                                       |

cal intron-exon on

A;Residues: 1-499 <WIR>
A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921
A;Genetics: AMY1
A;Accession: A33214
A;Accession: A33214
A;Accession: A33214
A;Accession: A32214
A;Rosidues: 1-499 <WI2>
A;Residues: 1-499 <WI2>
A;Rosidues: 1-499 <WI2>
A;Rosidues: 1-499 <WI2>
A;Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921
R;Genes, M.J.; Dove, M.J.; Seligy; V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing A;Reference number: JS0240; WUID:89378767; PMID:2789162

A;Rocession: 190.494
A;Rolecule type: DNA
A;Residues: 1-499 <GEN>
A;Rolecule type: DNA
A;Residues: 1-499 <GEN>
A;Rote: the authors refer to this as isozyme II
B;Isemura, S.; Ikenaka, T.
J. Baccession: A91330
A;Rote: the authors refer to this as isozyme II
R;Isemura, S.; Ikenaka, T.
J. Baccession: A91330
A;Reference number: A91330
A;Reference number: A91367
A;Residues: 206-225 <ISE>
R;Narita, K.
Proc. Jpn. Acad. S1, 285-290, 1975
A;Reference number: A93767
A;Reference number: A93767
A;Residues: 434-443,446-447,07,449-458,'GTTV',459-464,467-468,'B',470,'B',472-499 <NAR>
B;Residues: 434-433,446-447,07, 1949-458,'GTTV',59-464,467-468,'B', A70,'B',472-499 <NAR>
B;Residues: 434-433,446-447,07, 23, 1984
A;Residues: A34-433,446-447,07, 198-4212370, PNID:6609921
A;Reference number: A37454, MUID:84212370, PNID:6609921
A;Reference number: A37454, MUID:84212370, PNID:6609921
A;Reference number: A37454, MUID:84212370, PNID:6609921
A;Reference number: A37454, PDB:67AA
A;Contents: annotation; X-ray crystallography, 3.0 angetroms, residues 22-497
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics: AMY1>

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9 61 180

181

120 121 240

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Alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04549; A33215; Ā44713
R;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon on A;Reference number: S04548; MUID: 89237897; PMID: 2785629
A;Accession: S04549
A;Molecule type: DNA
A;Residues: 1-499 <WIR>
A;Accession: A33215
A;Accession: A33215
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A;Accession
A,Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A,Patkhway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase, alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIO>
F;22-49/Product: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
 KAAGVYCIGE LIDGDPAYTCPYQNVMDGVLNYPIXYPLLNAFKSTSGSMDDLYNMINTVK 300
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360
 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCPIQNYEDQTQ
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSODYFHPFCFIONYEDQTO
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 182 VEDCWLGDNTVSLPDLDTTKDVVKNEMYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKKVAAFIILNDGIPIIYAGOEOHYAGGND
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 TWQGIIDXLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
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 Length 499;
 Indele
 / Match 99.7%; Score 2675; DB 2; Local Similarity 99.8%; Pred. No. 3.1e-184; DB 497; Conservative 0; Mismatches 1;
 Query Match
Best Local Si
Matches 497
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 Aintrons: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
CiGenetics: <AMY2>
Aintrons: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
CiGenetics: <AMY2>
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CiFunction: Catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
Aiperstaption: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
Aiperstaption: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
Aiperstamily: Aspergillus alpha-amylase; alpha-amylase core homology
CiKeywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
F;21-29/Product: alpha-amylase core homology <AMY>
F;21-49/Product: alpha-amylase core homology <AMY>
F;1-59/17-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,211/Binding site: calcium (Asn. Glu. Asp. His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;217,251,318/Active site: Asp, Glu, Asp #status predicted
 RESULT 2

alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.

c;Species: Aspergillus sp.

c;Species: Aspergillus sp.

c;Date: 17-Mug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999

C;Accession: JS0663

R;Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.

Biosci. Biotechnol. Biochem. 56, 174-179, 1992

A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression A;Reference number: JS0663; MUID:92323146; PMID:1368777

A;Reselune: 1-499 <SHI>

C;Function:
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 420
 61 ŢWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNBNYGTADDL 121
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 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 241
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLINAFKSTSGSMDDLYNMINTVK 300
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360
 302 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGGEQHYAGGND 361
 421
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 480
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 19
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 2 MVAWWSLFLYGLQVAAPALAATFADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 PANREATWLSGYPIDSELYKLIASANAIRNYAISKDIGFVIYKNWPIYKDDTTIAWRKGT
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100.0%; Score 2684; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 7e-185;
Matches 498; Conservative 0; Mismatches 0; Indels 0
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N'Alternate names: Taka-amylase A
C;Species: Aspergilus oryzae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JND588
R;Tsukagoshi, N.; Furnkawa, M.; Nagaba, H.; Kirita, N.; Tsuboi, A.; Udaka, S.
Gene 84, 319-327, 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for mui
A;Reference number: JN0588; MUID:90128276; PMID:2612911
 two alpha-amylase genes from Asperc
 P. R. Korman, D. R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T. K. Korman, D. R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T. Curr. Genet. 17, 203-212, 1990
A,Fitle: Clonding, characterization, and expression of two alpha-amylase genes from A,Reference number: A48305, MUID: 90254827; PMID: 2340591
A,Reference number: A48305
A,Reference number: A8305
A,Reference number: A8305
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 122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
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 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 480
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 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
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 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
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 LIAMRKGI
 362 PANREATWLSGYPTDSELYKLIASRNAIRNYAISKDTGFVTYKOWPIYKODGTTIPMRKGT
 DGSOIVIILSNKGASGDSYILSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPVPMAGGLP
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 Gaps
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 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDD
 Length 499;
 Indels
 - Aspergillus oryzae
 Ouery Match 99.6%; Score 2674; DB 2; Best Local Similarity 99.6%; Pred. No. 3.7e-184; Matches 496; Conservative 0; Mismatches 2;
 alpha-amylase (EC 3.2.1.1) precursor
 481 RVLYPTEKLAGSKICSSS 498
 A, Accession: JN0588
A, Molecule type: mRNA
A, Residues: 1-499 <TSU>
A, Cross-references: UNIPROT: Q96TH4
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 RESULT 4
B48305
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C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGGEOHYAGGND
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 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
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 Length 499;
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 Indels
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 99.6%; Score 2674; DB 1;
99.6%; Pred. No. 3.7e-184;
iive 1; Mismatches 1;
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 RVLYPTEKLAGSKICSSS 498
 Best Local Similarity 99.6
Matches 496, Conservative
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Score 2662; DB 2; Pred. No. 2.7e-183; 0; Mismatches 2;

Length 498;

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182 VEDCWLGDNTVSLPDLDTTXDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 241
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 301
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C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
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 Query Match
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Matches 493; Conservative (
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C;Comment: The alpha amylases are encoded by multigene family.
C;Genetics:
A,Gene: Taa-G1
A,Gene: Taa-G1
A,Introns: $6/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
C;Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pescription: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pesthway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; polyasccharide degradation
C;Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <AIG>F;12-1/Domain: alpha-amylase eore homology <AMT>F;194-321/Domain: alpha-amylase core homology <AMT>F;194-321/Domain: alpha-amylase core homology <AMT>F;194-321/Domain: alpha-amylase (Asn) (covalent) #status predicted
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 420
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 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
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 CFINNYEDQTQ 180
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 TVQKDFWPGYN 240
 VEDCWLGDNTVSLPDLDTTXDVVXNEWYDWVGSLVSNYSIDGLRIDTVXHVQKDFWPGYN 241
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYP1YYPLLNAFKSTSGSMDDLYNMINTVK 300
 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 301
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 TWOGI I DKLDYI OGMGFTA I WITPVTA OLPOTTAYGDAYHGYWOODI YSLNENYGTADDL
 122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCLJQNYEDQTQ
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Best Local Similarity 99.6%; Pred. No. 4.3e-184;
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 RVLYPTEKLAGSKICSSS 498
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 RESULT 6
A48305
alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A83305
R;Corman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper A;Accession: A48305
A;Accession: A48305
A;Accession: A48305
A;Accession: A48305
A;Cossion: A48305
A;Cossion: A48305
A;Cossion: A48305
A;Cossion: A498
A;Cossion: A498
A;Cossion: A498
A;Cossion: Compared with conceptual translation
A;Molecule type: DNA
A;Cossion: Catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
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 RESULT 9
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 19
 alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N;Alternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JK0201
R;Toda, H.; Kondo, K.; Narita, K.
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAWRKGT
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
 CPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 TITKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 Gaps
 Gaps
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 478;
 Length 499;
 Length
 Query Match 93.3%; Score 2503.5; DB 2; Length Best Local Similarity 97.9%; Pred. No. 5.9e-172; Matches 468; Conservative 1; Mismatches 8; Indels
 Indels
site: His, Glu, Asp #status predicted
 C'Accession: JK0201
A.Toda, H.; Kondo, K.; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A.Title: The complete amino acid sequence of Taka-amylase
 Score 2656; DB 2;
Pred. No. 7.2e-183;
0; Mismatches 3;
 499
 RVLYPTEKLAGSKICSSS 498
 Query Match 99.0%;
Best Local Similarity 99.4%;
Matches 495; Conservative
 RVLYPTEKLAGSKICSSS
 VLDGDPAY
 SLPDLD
 VEDCWLGDNTA
 KAAGVYCIGE
F;231,251,318/Active
 242
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Alpha-amylase (EC 3.2.1.1) - Aspergillus niger
C; Species: Aspergillus niger
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C; Species: Aspergillus niger
C; Species: Aspergillus niger
C; Species: Aspergillus niger
C; Species: Aspergillus niger
C; Species: Aspergillus niger
C; Species: Aspergillus niger
R; Boel E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Petel
Biochemistry 29, 6.244-6249, 1990
A; Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom re
A; Reference number: A35282
A; Status: Aspecies in A35282
A; Status: preliminary, nucleic acid sequence not shown; not compared with conceptual tran
A; Status: preliminary, nucleic acid sequence not shown; not compared with conceptual tran
A; Status: 1484 < BOE>
C; Function:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pethway: glycopen/starch degradation
C; Superfamilly: Aspergillus alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaaccharide degradation
F; 173-300/Domain: alpha-amylase core homology < AMY>
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 140
 120
 200
 180
 260
 240
 320
 301 FASYINDIALAKAVAAFIILNDGLPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
 440
 361 LIASANAIRNYAISKDTGFVTYKN-PYIKDDTTIAMRKGTDGSQ1VTILSNKGASGDSYT 419
 123
 203
 241 PYONVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
 84 PVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHM 143
 183
 263
 83
 9
 63
 61 WITPVTAQLPQDCAYGDAYTGYWQTDIYSLNENYGTADDLKALSSALHERGMYLMYDVVA
 181 DVVKNEMYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
 DVV/KNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
 PYONVMDGVLNYPLYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT
 24 ADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWIT
 4 AEWRIQSIYFLLIDRFGRIDNSTTATCDTGDQIYCGGSWQGIINHLDYIQGMGFTAIWIS
 144 GYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVV
 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
 Gaps
 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
 ö
 Length 484;
 Indels
 93;
 Query Match 66.3%; Score 1780; DB 1;
Best Local Similarity 67.2%; Pred. No. 5.1e-120;
Matches 319; Conservative 63; Mismatches 93;
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RESULT 11
alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (Schwanniomyces occidentalis)
N;Alternate names: alpha-1,4 glucanohydrolase
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Species: Saja21
Curr. Genet. 24, 75-83, 1993
A;Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase from A;Reference number: Saja21; MUID:93365041; PMID:8358835
A;Reference number: Saja21; MUID:93365041; PMID:8358835
A;Reference number: Saja21
A;Molecule type: DNA
A;Residues: 1-507 < CLA>
A;Residues: 1-507 < CLA>
A;Residues: 1-507 < CLA>
A;Residues: 1-507 < CLA>
A;Residues: 1-507 < CLA>
A;Residues: 1-507 < CLA>
C;Superiami: Siga2
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase; polyaaccharide degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase; sore homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polyaaccharide degradation
F;1-20/Domain: signal sequence #status predicted <AMT>
F;20-500/Product: alpha-amylase core homology <AMX>
F;21-500/Product: alpha-amylase core homology <AMX>
F;21-500/Product: alpha-amylase core homology <AMX>
F;21-500/Product: alpha-amylase core homology <AMX>
F;21-500/Pomain: signal sequence #status predicted <AMX>
F;21-500/Pomain: signal sequence #status predicted <AMX>
F;21-500/Pomain: signal sequence #status predicted <AMX>
F;21-500/Pomain: alpha-amylase core homology <AMX>
F;21-500/Pomain: alpha-amylase core homology <AMX>
F;21-500/Pomain: alpha-amylase core homology <AMX>
F;21-500/Pomain: alpha-amylase core homology <AMX>
F;21-500/Pomain: alpha-amylase core homology <AMX>
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F;21-500/Pomain: alpha-amylase core homology <AMX>
F;21-500/Pomain: alpha-amylase core homology <AMX>
F;21
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 501
 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
 253 SAAGVYLLGEVYDGDPAYTCPYQNYMSGVTNYPLYYPMLRFFGGTSNSVDELNAMISSLE 312
 315 NHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPT 374
 434
 561
 494
 621
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
322 DVNTQLDTVKSEYQSWVKQLIANYSIDGLRIDTVKHVQMDFWAPFQEAAGIYTVGEVFDG 381
 9
 72
 DPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVE
 442 NQDNPRFPSYTSDESLIKNATAPTILSDGIPIIYYGQEQGLNGGNDPYNREALMPTGYST
 DSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGA
 SGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKI
 562 SGSSYTLTLSNTGYTASSVVYEILTCTAVTVDLSGNLAVPMSGGLPRVFYPESQLVGSGI
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 Gaps
 Length 507;
 56.9%; Score 1527; DB 2; Length 557.7%; Pred. No. 7.8e-102; ive 74; Mismatches 130; Indels
 Best Local Similarity 57.77
Matches 286; Conservative
 Local Similarity
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 A; Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages A; Description: hydrolyzes raw starch, degradation C; Superfamily: Ilpomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch C; Superfamily: Lipomyces alpha-amylase; alpha-amylase starch C; Keywords: extracellular protein; glycoptotein; glycosidase; hydrolase; polysaccharide F; 12-28/Domain: signal sequence #status predicted <SIG>F; 12-28/Domain: alpha-amylase starch-binding domain homology <SBD>F; 320-447/Domain: alpha-amylase core homology <AMY>F; 320-447/Domain: alpha-amylase core homology <AMY>F; 330-447/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 334, 344/Active site: His, Glu, Asp #status predicted
 A;Cross-references: UNIPROT:Q01117; GB:U30376; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A;Experimental source: strain IGC4052B
A;Accession: PC4116
 a Lipd
 NyAlternate names: LKAI protein, raw starch-degrading amylase
NyContains: alpha-dextrin endo-1,6-alpha-glucosidase (BC 3.2.1.41)
Cispecies: Lipomyces kononenkoae
Cispecies: Lipomyces kononenkoae
Cispecies: Lipomyces kononenkoae
Cispecies: Lipomyces kononenkoae
Cispecies: Lipomyces kononenkoae
Cispecies: Lipomyces kononenkoae
Cispecies: Lipomyces kononenkoae
Cispecies: Lipomice appliante Laboration (Cispecies)
Cispecies: Lipomice (Cispecies)
Alitha: Cloning, sequence analysis and expression in yeasts of a cDNA containing A; Reference number: UC4510; WUID:96105202; PMID:8529895
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 383
 303
 443
 423
 134
 202 MGFTAIWISPIVENIPDDTGYGYAYHGYWMKDIPALNTNFGGADDLIALATELHNRGMYL 261
 262 MVDIVVNHFAFSGNHADVDYSEYFPXSSQDYFHSFCWITDYSNQTNVEECWLGDDSVPLV 321
 DLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDG 254
 RTIWYDWVADLVSNYSVDGLRIDSVLEVEPDFFPGYQEAAGVYCVGEVDNGNPALDCPYQ 243
 142 SASVPTGTAANWRGRSIYQVVTDRFARTDGSITYSCDVTDRVYCGGSYRGIINMLDYIQG 201
 MYDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLP 194
 74
 244 KVLDGVLNYPTYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPRFAS
 YTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIA
 SANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSL
 MGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYL
 NVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFAS
 AAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQG
 Gaps
 SGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
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 pullulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
 DB 1; Length 624;
 / Match 60.7%; Score 1629; DB 1; Length 62 Local Similarity 60.6%; Pred. No. 5e-109; nes 292; Conservative 77; Mismatches 113; Indels
 A, wccession: PC4116
A, Molecule type: protein
A, Residues: 29-44 <5T2>
A, Experimental source: IGC4052B
C, Genetics:
A, Genetics:
C, Funcri---
 A; Molecule type: mRNA
A; Residues: 1-624 <STE>
 364
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 135
 264
 324
 384
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alpha-amylase (EC 3.2.1.1) precursor - yeast (Saccharomycopsis fibuligera)
C.Species Saccharomycopsis fibuligera
C.Species 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C.Accession: S00064
C.Accession: S00064
T.; Yamashita, I.; Fukui, S.
FEBS Lett. 219, 339-342, 1987
A.;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycops
 A;Accession: S23355
A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rosiduss: 1-512 <WUF>
A;Cross-references: UNIPROT:P19269; EMBL:X62079; NID:g4880; PIDN:CAA43995.1; PID:g4881
A;Cross-references: UNIPROT:P19269; EMBL:X62079; NID:g4880; PIDN:CAA43995.1; PID:g4881
A;Note: the authors translated the codon AGA for residue 21 as Pro, CTT for residue 61
C;Superfamily: Aspergillus alpha-amylase; Alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase
F;209-336/Domain: alpha-amylase core homology <AMY>
 alpha-amylase (EC 3.2.1.1) precursor - yeast (Schwanniomyces occidentalis) C;Species: Schwanniomyces occidentalis C;Species: Schwanniomyces occidentalis C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S23355 R;Wu, F.M.; Mang, T.T.; Hsu, W.H. A;FEMS Microbiol. Lett. 82, 313-318, 1991 A;Title: The nucleotide sequence of Schwanniomyces occidentalis alpha-amylase gene. A;Reference number: S23355
 ä
 445
 265
 402 NQIRNQAIKKDSAYSTYKSSVVSSSDHYIATRKGSDANQLISIFNNLGSNG-SQDITVSN 460
 101
 86 TAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMGY 145
 325
 282 MKGVINYPLYYPVYRFFSDTSAISSELTSMISTLQSSCSDVSLLGNFIENHDQVRFPSVT 341
 NDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIASA 385
 ELISKLNQIRNQAIKKDSAYSTYKSSVVSSSDHYIATRKGSDANQLISIFNNLGSNG-SQ 454
 222 VFQTWVSDFVQNYSIDGLRIDSAKHVDTASLTKFEDASGVYNLGEVYQGDPTYTCPYQSY 281
 82
 511
 DGAGSSVDYSVPKPPSSQDYFHPPCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKN
 26 WRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITPV
 EWYDWVGSLVSNYSIDGLRIDTVXHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQNV
 MDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYT
 386 NAIRNYAISKDIGFVIYKNWPIYKDDITIAMRKGIDGSQIVTILSNKGASGDSYTLSLSG
 440 TLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS
 DITVSNTGYSSGDKVIDIISCNSVLAGDSGSLSVSISGGMPQVYAPSSVLSGSGICN
 ;
 512;
 461 TGYSSGDKVIDIISCNSVSAGDFGSLSVSISGGMPQVYAPSSVLSGSGICN
 446 AGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS
 Length
 Indels
 5
 56.5%; Pred. No. 5.6e-96; ive 74; Mismatches 130;
 DB
 53.9%; Score 1445.5;
 Local Similarity 56.5% tes 266; Conservative
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 326
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 October anylase (EC 3.2.1.1) AMY1 precursor - yeast (Schwanniomyces occidentalis)
C; Species: Schwanniomyces occidentalis
C; Species: Schwanniomyces occidentalis
C; Species: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C; Accession: S06115
R; Strasser, A.W.M.; Selk, R.; Dohmen, R.J.; Niermann, T.; Bielefeld, M.; Seeboth, P.; Tu
Eur. J. Biochem. 184, 699-706, 1989
A; Title: Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secre
A; Reference number: S06115; MUD:90032659; PMID:2806251
A; Molecule type: DNA
A; Residues: 1-512 <STR>
A; Molecule type: DNA
A; Residues: 1-512 <STR>
A; Cross-references: UNIPROT:P19269; EMBL:X16040; NID:94882; PIDN:CAA34162.1; PID:94883
C; Gene: AMY1
C; Function:
A; Gene: AMY1
C; Function:
A; Gene: AMY1
C; Function:
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C; Function:
A; Gene: AMY1
C; Superfamily: Aspergillus alpha-amylase; Japha-amylase core homology in Files Domain: signal sequence #status predicted <SIG>F; Reywords: glycoprotein; glycosidaes; hydrolase; polysaccharide degradation
F; 1-57 Domain: signal sequence #status predicted <AMT>
F; 209-336/Domain: alpha-amylase core homology <AMX>
E; 209-336/Domain: alpha-amylase core homology <AMX>
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E; 209-336/Domain: Amylase core homology <AMX>
E; Apple Amylase Amylase Core homology <AMX>
E; Amylase
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 SDCKDITLLGNFIENHDQPRLPSYTSDSALIKNAIAFNLMSDGIPIIYYGGEGGYSGSSD 372
 YNHYAWNGDGSSVDYSSFTPFNQQSYFHDYCLITNYNDQTNVEDCWEGDTEVSLPDLSTE 215
 DNEVIGVEQTWVSDFVQNYSIDGLRIDSAKHVDTASLITKFEDASGVYNLGEVYQGDPTYT 275
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKOWPIYKDDTTIAMRKGT 420
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 480
 IWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVV 139
 ANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTT 199
 CPYONVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNP 319
 RFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELY 379
 KLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSY 439
 79
 95
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 KDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYT
 21 ATPAD-WRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTA
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 5
 512;
 54.0%; Score 1449; DB 2; Length 5
56.4%; Pred. No. 3.1e-96;
ive 74; Mismatches 132; Indel8
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 A, Forestdues: 1-494 (ITC)
A, Cross-references: UNIPROT: P21567; EMBL: X05791; NID: 94847; PIDN: CAA29233.1; PID: 94848
A, Octoss-references: UNIPROT: P21567; EMBL: X05791; NID: 94847; PIDN: CAA29233.1; PID: 94848
A, Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Thr C; Genetics:
A, Genetics:
 alpha-amylase (EC 3.2.1.1) precursor - Cryptococcus sp. (strain CS2)

c.Species Cryptococcus sp.
A;Variety: strain CS2)
C;Species Cryptococcus sp.
C;Species: 23-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: S72270
C;Accession: S72270
A;Variety: A; Kato, M.; Iimura, Y.
Biochem. J. 318, 998-996, 1996
A;Title: Raw-starch-digesting and thermostable alpha-amylase from the yeast Cryptococcus
A;Reference number: S72270; MUID:96433120; PMID:8836148
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 353
 301 QMISSVASSCSDPTLLTNFVENHDNERFASMTSDQSLISNAIAFVLLGDGIPVIYYGQEQ 360
 361 GLSGKSDPNNREALWLSGYNKESDYYKLIAKANAARNAAVYODSSYATSOLSVIFSNDHV 420
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 NYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQK 233
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 354 HYAGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKWWPIYKÜDTT 413
 23
 9
 12 LQVAAPALAA-------TPAD-WRSQSIYFLLTDRFARTDGSTTATCNTA
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 Gaps
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 474 PMAGGLPRVLYPTEKLAGSKICS 496
 A; Molecule type: DNA
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 186
 306 QLAQGISAMQSDCSDTTLLGSFLENQDNPRFPSQTSDLTRAQNALAFTMLQDGIPITYYG 365
 425
 467
 IIDKLDYIQGMGFTAIWITPVTAQLP----QTTAYGDAYHGYWQQDIYSLNENYGTADD 119
 LKALSSALHERGMYLMVDVVANHMGY-----DGAGSSVDYSVFKPFSSQDYFHPFCFI 172
 173 QNYEDOTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQ 232
 KDFWPGYNKAA-GVYCIGEVLDGDPAYTCPYQNV-MDGVLNYPIYYPLLNAFKSTSGSMD 290
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 9 LYGLQVAAPALAA - TPADWRSQSIYFLLTDRFARTDGSTTATCNTADQ - KYCGGTWQG
 DDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLSGA--GYTAGQQLTEVIGCTTVTVGS
 Gaps
 22;
 47.1%; Score 1264; DB 2; Length 6 ilarity 49.2%; Pred. No. 8e-83; Conservative 84; Mismatches 153; Indels
 DGSLSFTMTGGLPRVFYNATALAESSLCTT
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February 8, 2005, 18:25:28 ; Search time 292.263 Seconds (without alignments) 872.556 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 OM protein - protein search, using sw model
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US-10-820-200-2
2684
1 MVAWWSLFLYGLQVAAPALA......LPRVLYPTEKLAGSKICSSS 498 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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 Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Udaka S., "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple related genes.";
Gene 84:319-327(1989).
 [3]
SEQUENCE FROM N.A.
Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
"Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
 MEDLINE-89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6; Genes M.J., Dove M.J., Seligy V.L.; "Aspergillus oryzae has two nearly identical Taka-amylase genes, each Gene Introns."; introns."; Gene 79:107-117(1989).
 SEQUENCE OF 206-225.
MEDLINE=14001521; PubMed=4733850;
ISEMURE=X. IKenaka T.;
"The amino acid sequences of glycopeptides obtained from Taka-amylase A with trypsin and chymotrypsin.";
 361 PANREATWLSGYPTDSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGT
 DGSO1VT1LSNKGASGDSYTLSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPVPMAGGLP
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 AWYA ASPOR STANDARD; PRT; 499 AA.
P10529; P11763; Q00250;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-alpha-D-glucan glucanohydrolase).
 Eukaryota, Pungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
 SEQUENCE FROM N.A.
MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
 Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.,
"Three alpha-amylase genes of Aspergillus oryzae exhibit identical
intron-exon organization.";
Mol. Microbiol. 3:3-14(1989).
 Toda H., Kondo K., Narita K., "The complete amino acid sequence of Taka-amylase A."; Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982)
 Aspergillus oryzae.";
Agric. Biol. Chem. 53:593-599(1989).
 STRAIN=DSM 63303;
MEDLINE=89237897; Pubmed=2785629;
 RVLYPTEKLAGSKICSSS 498
 RVLYPTEKLAGSKICSSS 498
 [5]
SEQUENCE OF 22-499.
 Aspergillus oryzae.
 [2]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=5062;
 Name=AMY1;
 Name=AMY2;
 Name=AMY3;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 at high concentrations.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

SUDICATION/COST: Used in the brewing industry to increase the fermentability of beer worts (including those made from unmalted cereals), in the starch saccharification, in the alcohol industry to reduce fermentation time, in the cereal food industry for reduce fermentation and improvement of chilled and frozen dough, and in the forsetry industry for low-temperature modification of starch. Sold under the name Fungamyl by Novozymes.

MISCELLANBOUS: The sequence of AMYl and AMY2 is shown.

SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 MEDLINE=80227691; PubMed=6156152;
Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
"Molecular structure of taka-amylase A. I. Backbone chain folding at
3-A resolution."
 3D-structure; Calcium-binding; Carbohydrate metabolism; birdet protein sequencing; Glycoprotein; Glycosidase; Hydrolase; Multigene family; Signal. SIGNAL
 MEDLINE=84212370; PubMed=6609921;
Matguura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Blochem. 95:697-702(1984).
 Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975)
 Alpha-amylase A.
 InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; I.
PRINTS; PR00110; ALPHAAMYLASE.
 X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 Biochem. 87:1555-1558(1980).
 EMBL; X12725; CAA31218.1; --
EMBL; X12726; CAA31219.1; --
EMBL; X12727; CAA31220.1; --
EMBL; M3218; BAA0336.1; --
EMBL; M3318; AAA32708.1; --
EMBL; M3218; AAA32708.1; --
PIR; JV0201; JV0201.
PIR; JV0466; JT0466.
PIR; S04548; ALAS1.
PDB; STAA; X-ray; @=22-499.
PDB; GTAA; X-ray; @=22-499.
PDB; TTAA; X-ray; @=22-499.
J. Biochem. 74:1-10(1973)
 GlycoSuiteDB; P10529; -.
 SEQUENCE OF 433-499.
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61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
 62 TWQGIIDKLDYIQGMGFTAIMITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 302 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTBVIGCTTVTVGSDGNVPVPMAGGLP
 Gaps
 Alpha-amylase precursor.

Name-amyl 1;
Aspergillus awamori.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

NCBI_TaxID=105351;
 ö
 Length 499
 STRAIN=KT-11;

A Matsubara T.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases

R MOS GO: 0004556; F:alpha-amylase activity; IEA.

R GO; GO: 0004556; P:carbohydrate metabolism; IEA.

R GO; GO: 0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR0065047; Alpha amyl cat.

R InterPro; IPR0065046; Alpha amyl cat.

R InterPro; IPR0065046; Alpha amyl cat.

R Pfam; PF00128; Alpha-amylase; 1.

R Pfm; PF00128; Alpha-amylase; 1.

R Pfintry; PR00110; Alpha-Amylase; 1.
 Indela
 21 Potential.
54794 MW; 2B357AE38B36C1C2 CRC64;
 Created)
Last sequence update)
Last annotation update)
 DB 1;
 100.0%; Score 2684; DB 1
100.0%; Pred. No. 2e-178;
ive 0; Mismatches 0
 499 AA
 481 RVLYPTEKLAGSKICSSS 498
 076L99;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 100.
Matches 498; Conservative
 PRELIMINARY;
 SMART; SM00642; Aamy; 1.
Signal.
SIGNAL 1 21
SEQUENCE 499 AA; 5479
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SEQUENCE FROM N.A.
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 Calcium 1.
Calcium 1 (via carbonyl oxygen).
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/FTId=cAR_000125.
P -> R (in AMY3).
F -> L (in AMY3).
TT -> DC (in Ref. 5).
O -> T (in Ref. 5).
O -> Y (in Ref. 3).
P -> L (in Ref. 3).
G -> V (in Ref. 3).
I -> L (in Ref. 3).
I -> L (in Ref. 3).
I -> L (in Ref. 4).
I -> L (in Ref. 5).
I -> L (in Ref. 5).
C -> A (in Ref. 5).
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C -> S (in Ref. 5).
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or send an email to license@isb-sib.ch).
 Alpha-amylase
 499
 RVLYPTEKLAGSKICSSS 498
 EMBL; D10461; BAA01255.1; -.
 RVLYPTEKLAGSKICSSS
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499 AA;
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 240
 120
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 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
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 302 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 361
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 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
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 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWFDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 362 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 MEDLINE=92333146; PubMed=1368777; Mara S.; MEDLINE=92333146; PubMed=1368777; Mera S.; MEDLINE=92333146; PubMed=1368777; Mera S.; Medline Spirousamii and its Shibuya I., Tamura G., Ishikawa T., Hara S.; Cloning of the alpha-amylese CDNA of Aspergillus shirousamii and its expression in Saccharomyces cerevisiae."; Piotechnol. Biochem. 56:174-179(1992).

-I. CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

-I. CORCTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).

-I. SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5070;
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 Length 499;
 Indels
 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
99.9%; Score 2680; DB 2; 99.8%; Pred. No. 3.9e-178; iive 1; Mismatches 0;
 499 AA
 RVLYPTEKLAGSKICSSS 498
 RVLYPTEKLAGSKICSSS 499
 Best Local Similarity 99.8
Matches 497, Conservative
 STANDARD;
 Aspergillus shirousami
 glucanohydrolase).
Name=AMY;
 AMY_ASPSH
P30292;
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ö 180 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGKN 241 242 KAAGVYCIGEVLDVDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLXNMINTVK 301 361 420 480 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 121 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360 421 481 9 61 2 MYAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQXYCGG TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNBNYGTADDL 302 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGGEQHYAGGND KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCF1QNYEDQTQ PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG Interproj 1970 (1980)
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Interproj 1970 (1980) Gaps .) (By similarity) (By (B ô / Match 99.7%; Score 2675; DB 1; Length 499; Local Similarity 99.8%; Pred. No. 8.6e-178; nes 497; Conservative 0; Mismatches 1; Indels

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PRELIMINARY;
 SEQUENCE FROM N.A. STRAIN-RIB40;
 Name=amyA;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for chamercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 SERVENTE FACT.

STRAIN-UK141F;

MEDLINE=90254827; PubMed=2340591;

KOTMAN D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,

KOTMAN D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,

ROYET T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;

"Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus niger var. awamori.";

Curr. Genet. 17:203-212(1990).

-!-CATALYITC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

-!-CATALYITC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

-!-CATALYITC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

-!-COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory

at high concentrations (By similarity).

-!-SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
 Aspergillus awamori.
Sukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=105351;
 similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
 (B
 .) (Potential)
 Alpha-amylase B.
Nucleophile (By similarity).
Proton donor (By similarity).
By similarity.
Calcium 1 (By similarity).
Calcium 1 (by similarity).
 99.6%; Score 2674; DB 1; Length 499; 99.6%; Pred. No. 1e-177; tive 0; Mismatches 2; Indels (
 01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 .iinked (GlcNAc. . .) (Pc
740B96B11BC01A8A CRC64;
 By similarity.
By similarity.
N-linked (GlcNAc.
 499
 Potential.
 InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; I.
PRINTS; PR00110; ALPHAAMYLASE.
 54921 MW;
 EMBL; X52756; CAA36967.1; -.
PIR; B48305; B48305.
HSSP; P10529; 7TAA.
 Query Match
Best Local Similarity 99.6
Matches 496; Conservative
 STANDARD;
 227
251
318
142
183
 251
59
185
304
496
218
 251
51
171
261
461
218
499 AA;
 glucanohydrolase B)
Name=AMYB;
 SEQUENCE FROM N.A.
 251
318
142
183
 AMYB ASPAW
Q02906;
 METAL
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Gaps

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480
 120
 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 121
 180
 181
 240
 241
 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
 301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360
 302 SDCPDSTLLGTFVENHDNPRFASYTNDIALARAVVAAFIILANDGIPIIYAGQEQHYAGGND 361
 361 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT 420
 421
 422 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 481
 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 301
 61
 "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
421 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
 182 VEDCWIGDNITVSLPDLDITXDVVKNEWYDWVGSLVSNYSIDGLRIDIVKHVQKDFWPGYN
 362 PANREATWLSGYPTDSELYKLIASRNAIRNYAISKDTGFVTYKNWPIYKDDTTIPMRKGT
 TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 on glycosyl bonds; IEA.
 Aspergilus oryzae.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=5062,
 MEDLINE=20289310; PubMed=10830498;
Gomi K., Kumagai C., Okazaki N.,
Iimura Y.;
 Toryzac.";

Disosci. Biotechnol. Biochem. 64:816-827(2000).

C. -!- SIMILMARIY: Belongs to family 13 of glycosyl hydrolases.

EMBL, AB021876; BAA95703.1; -..

EMBL, AB024876; BAA95703.1; -..

R PIR; JN0588; JN0588.

R PIR; OG4549; ALAS3.

R GO; GO:0004556; F:alpha-amylase activity; IEA.

R GO; GO:0004556; F:hydrolase activity, acting on glycosyl bonds; R GO; GO:0005795; P:carbohydrate metabolism; IEA.

R InterPro; IPR006689; Alpha amyl.cat.

R InterPro; IPR006689; Alp_amyl.cat.

R InterPro; IPR006046; Glyco_hydro_lyd
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Taka-amylase A (EC 3.2.1.1).
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 499
 481 RVLYPTEKLAGSKICSSS 498
 482 RVLYPTEKLAGSKICSSS 499
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us-10-820-200-2.rup

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Pfam; PF00128; Alpha-amylase; 1.
 99.6%;
 Local Similarity 99.6 tes 496; Conservative
 glucanohydrolase A).
Name=AMYA;
 SEQUENCE FROM N.A.
 241
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 Query Match
 AMYA_ASPAW
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 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
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 182 VEDCWLGDNIVSLPDLDITKDVVKNEWYDWVGSLVSNYSIDGLRIDIVKHVQKDFWPGYN 241
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 361
 420
 421
 480
 481
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 61
 [1] _
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANI=86-10D;
Fakhoury A.M., Woloshuk C.P.;
Fakhoury A.M., Woloshuk C.P.;
T "Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in aflatoxin biosynthesis in maize kernels.";
T aflatoxin biosynthesis in maize kernels.";
Phytopathology 89:908-914(1999).
C -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
R EMB1, AR13925; ARF13642.1, -.
R GO; GO:0016798; F:Alpha-amylase activity; IEA.
R GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
R GO; GO:0005975; P:carbohydrate metabolism; IEA.
R InterPro; IPR006699; Alpha_amyl_cat.
R InterPro; IPR006699; Alp_amyl_cat.
R InterPro; IPR006696; GlyCo_hydro_l3.
 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 PANREATWLSGYPTDSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGT
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 Gaps
 Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 ..
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 Length 499;
 99.6%; Score 2674; DB 2; Length 4 99.6%; Pred. No. 1e-177; rative 1; Mismatches 1; Indels
 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
 Created)
Last sequence update)
Last annotation update)
 499 AA
 RVLYPTEKLAGSKICSSS 498
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Alpha-amylase (EC 3.2.1.1).
 Matches 496; Conservative
 SMART; SM00642; Aamy; 1.
 PRELIMINARY;
 Glycosidase, Hydrolase.
SEQUENCE 499 AA; 548
 Aspergillus flavus.
 Local Similarity
 NCBI_TaxID=5059;
 Q7LV45;
05-JUL-2004 (
05-JUL-2004 (
 Name=amy1;
 121
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 181
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 242
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 Query Match
 Q7LV45
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 TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
 121
 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
 181
 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
 301
 361
 61
 Modern D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
"Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus niger var. awamori.";
Curr, Genet. 17.203-212(1990).
-!- CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
-!- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINIVK
 SDCPDSTLLGTFVENHDNPRFASYTNDIALARAVVAAFIILNDGIPIIYAGQEQHYAGGND
 2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADRKYCGG
 SDCPDSTLLGTFVENHDNPRFASYINDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 PANREATWISGYPIDSELYKLIASANAIRNYAISKDIGFUTYKOWPIYKODTIIAMRKGT
 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 PANREATWLSGYPIDSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKODITIAMRKGT
 Gaps
 Aspergillus awamori.
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
 ö
 499;
 AMYA ASPAW STANDARD; PRT; 498 AA.
002905;
01-00T-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 35, Last annotation update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase A precursor (BC 3.2.1.1) (1,4-alpha-D-glucan
 Score 2674; DB 2; Length 4
Pred. No. 1e-177;
1; Mismatches 1; Indels
PRINTS; PR00110; ALPHAAMYLASE.
SWART; SM00642; Aamy; 1.
Glycosidase; Hydrolase
SEQUENCE 499 AA; 54804 WW; EEF42ADA71D20DA9 CRC64;
 STRAIN=UVK143F;
MEDLINE=90254827; PubMed=2340591;
 RVLYPTEKLAGSKICSSS 498
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422 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPWAGGLP 481
 252 LDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGT 311
 FQGDPDYTCGYQEVMDGVLNYPIYYPLLRAFSSTSGSLSDLANMIETVKYTCSDATLLGN 304
 432 KGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAG 491
 185 SLPDVDTTNEEVKEIMYDWVGDLVSDYSIDGLRIDTARHVQKDFWRDYNDAAGVYCVGEV
 72 IQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERG
 MYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYPHPFCFIQNYEDQTQVEDCWLGDNTV
 192 SLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEV
 372 YPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSN
 12 LQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDY
 Bodge N.A., Murphy R.M., Kelly J.M.;

Bodge N.A., Murphy R.M., Kelly J.M.;

L. Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

R. EMBL, AP708225; AP17103.1;

R. HSSP; P10529; 7TAA.

R. GO; GO:0004525; F:alpha-amylase activity; IEA.

R. GO; GO:0005975; P:carbohydrate metabolism; IEA.

R. InterPro; IPR00647; Alpha_amyl_cat_sub.

R. InterPro; IPR006589; Alpha_amyl_cat_sub.

R. InterPro; IPR006589; Alpha_amyl_cat_sub.

R. Frintry; PR00110; Alpha_amylase; 1.

R. SWART; SM00642; Amy; 1.

SSMART; SM00642; Amy; 1.

SSEQUENCE 490 AA; 54249 MW; A891C4ACEAEBS305 CRC64;
 Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
 Query Match 68.0%; Score 1826; DB 2; Length 490; Best Local Similarity 69.6%; Pred. No. 1e-118; Matches 337; Conservative 53; Mismatches 92; Indels
 Last sequence update)
Last annotation update)
 Created)
 481 RVLYPTEKLAGSKIC 495
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
 -PRELIMINARY;
 Alpha-amylase AmyA.
 SEQUENCE FROM N.A.
 Name=amyA;
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 245
 421
 Q9UV07
 RESULT 9
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 240
 300
 360
 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEbQTQ 180
 420
 KALSSALHERGMYLAVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIXYPLLINAFKSTSGSMDDLYNMINTVK 301
 61
 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSI DGLRI DTVKHVQKDFWPGYN
 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
 SANATHANYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
 Gaps
 EMBL; X52755; CAA16966.1; -.

P.TR; A48305; A48305.

HSSP; P10529; 7TAA.

InterPro; IPR006047; Alpha amyl cat.

InterPro; IPR006047; Alpha amyl cat.

InterPro; IPR006046; Glyco_hydro_13.

Prin; PR00128; Alpha-amylase; 1.

PRINTS; PR00110; AlphAAMYLASE.

SMART; SM00642; Aamy; 1.

Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase; Signal.

SIGNAL.
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 -linked (GlcNAc. ..) (Potential) 7658511BC01A8A01 CRC64;
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 (By similarity).
(By similarity).
(via carbonyl oxygen).
 Nucleophile (By similarity).
Proton donor (By similarity).
By similarity).
By similarity).
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
 99.2%; Score 2662; DB 1; Length 498; 99.6%; Pred. No. 6.9e-177;
at high concentrations (By similarity). SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 2; Indels
 (By similarity)
 Alpha-amylase A.
 similarity).
Calcium 1 (By Calcium 2 (By Calcium 2 (By Similarity).
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By Similarity.
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By Similarity.
By Similarity.
 0; Mismatches
 PANREATWLSGYPTDSELYKLI
 54880 MW;
 Best Local Similarity .v. Matches 493; Conservative
 251
59
185
304
496
218
 196
227
231
 498 AA;
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318
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 TAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVD 137
 TTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPA 257
 258 YTCPYQNVMDGVLNYPIXYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHD 317
 VVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLD 197
 318 NPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSE 377
 78
 LDCPYQDYLDGVLNYPIYMQLLYAFESSGSISDLYNMIKSVASDCSDPTLLGNFIENHD
 378 LYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGD
 379 LYTWIATTNAIRKLAISADSDYITYKNDPIYTDSNTIAMRKGTSGSQIITVLSNKGSSGS
 438 SYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSS
 19 ALGLSAAEWRSQSIYFLLTDRFGRTDNSTTATCDTGDQIYCGGSWQGIINHLDYIQGMGF
 ALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGF
 Gaps
 Aspergillus awamori.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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 634;
 A Matsubara T.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Is Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; AB083162; BAD06003.1; -.
R HSSP; P04064; 1ACZ.
R GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005924; F:catalytic activity; IEA.
R GO; GO:0005975; P:catalytic activity; IEA.
R GO; GO:0005975; P:catalytic activity; IEA.
R InterPro; IPR006047; Alpha_amyl_cat.
R InterPro; IPR006047; Alpha_amyl_cat.
R InterPro; IPR002044; Glyco_hydro_GBD.
R Ffam; PF00128; Alpha-amylase; 1.
R Pfam; PF00128; Alpha-amylase; 1.
R Pfam; PF00188; GBM 20; 1.
 Query Match 66.7%; Score 1791; DB 2; Length 6 Best Local Similarity 68.6%; Pred. No. 3.9e-116; Matches 321; Conservative 64; Mismatches 83; Indels
 1 21 Potential.
634 AA; 69242 MW; 16C0BE6AF6FB0E9B CRC64;
 Last sequence update)
Last annotation update)
 Potential
 Created)
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 PRELIMINARY;
 Alpha-amylase precursor.
Name=amyl III;
 SMART; SM00642; Aamy; 1.
Signal.
 NCBI_TaxID=105351;
 SEQUENCE FROM N.A.
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78 TAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVD 137
 138 VVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLD 197
 TIKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPA 257
 258 YTCPYQNVMDGVLNYPLYYPLLNAPKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHD 317
 259 LDCPYQKYLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHD 318
 77
 19 ALGLSAAEWRTQSIYFLLTDRFGRTDNSTTATCNTGDQIYCGGSWQGIINHLDYIQGMGF 78
 18 ALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGF
 Kaneko A., Sudo S., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.; "Molecular-cloning and determination of the nucleotide-sequence of a gene encoding an acid-stable alpha-amylase from Aspergillus-
 Gaps
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Acid-stable alpha-amylase.
Aspergillus kawachi (Aspergillus awamori var. kawachi).
Eukaryota; Rungl; Ascomycota; Pazizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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 90; Indels
 Kaneko A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABA003170; BAA22993.1; --
HSSP; P56271; 2AAA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0005824; F:catalytic activity; IEA.
GO; GO:0005975; P:catalytic activity; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006089; Alp_amyl_cat.
InterPro; IPR006089; Alp_amyl_cat.
InterPro; IPR002044; GlyCo_hydro_CBD.
 Length
 69507 MW; 676BF9D0236720DD CRC64;
 67.4%; Score 1810; DB 2;
67.6%; Pred. No. 1.9e-117;
ive 66; Mismatches 90;
 Pfan, PP00128; Alpha-amylase; 1.
Pfan; PP00686; CBM 20; 1.
ProDom; PD001568; Glyco_hydro_CBD; 1.
 J. Ferment. Bioeng. 81:292-298(1996). [2]
SEQUENCE FROM N.A.
 Matches 325; Conservative
 PRELIMINARY;
 SMART; SM00642; Aamy SEQUENCE 640 AA;
 Best Local Similarity
 SEQUENCE FROM N.A.
 492 SKIC 495
 SGIC 488
 NCBI_TaxID=40384;
 kawachii.";
 198
 Query Match
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Length 484;
 52935 MW; 04D596E34680656D CRC64;
 DB 1;
 Score 1778;
 66.2%;
 SEQUENCE
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RAY MINITES-9100214; PubMed-2207056;

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RAY GRAY L. Petersen S.B., Swift H., Thim L., Moldke H.P.; Cancium binding in alpha anglases an X ray diffrraction study at 2.1-R. Cancium binding in alpha anglases an X ray diffrraction study at 2.1-R. CATALLYTY: Endonydrolysis of I,4-alpha-glucosidic L. CATALLYTY: Endonydrolysis of I,4-alpha-glucosidic L. CATALLYTY: Endonydrolysis of I,4-alpha-glucosidic L. CATALLYTY: Endonydrolysis of I,4-alpha-glucosidic L. CATALLYTY: Endonydrolysis of I,4-alpha-glucosidic L. CATALLYTY: Endonydrolysis of L. Calcium is inhibitory at high concentrations.

C. CATALLYTY: Belongs to the glycosyl hydrolase 13 family.

BE RAY CATALLYTY: Belongs to the glycosyl hydrolase 13 family.

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RAY SAN
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 46, Last annotation update)
Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase)
Aspergillus niger.
Eukaryota, Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5061;
 484 AA
 AWYA ASPNG
AMYA ASPNG
AMYA ASPNG
AMYA ASPNG
ACC PS6271;
DT 15-UUL-1998
DT 25-OCT-2004
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RX MEDLINE-910
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250 IFHGDPAYTCPYQDYMDGVMNYPIXYPLLNAFKSSSGSMSDLYNMINTVASNCRDPTLLG 309
 311 TFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLS 370
 371 GYPIDSELYKLIASANAIRNYAISKDIGFVIYKNWPIYKDDTTIAMRKGIDGSQIVTILS 430
 431 NKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLA 490
 LQVAAPALAATPAD-WRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLD
 YIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHER
 131 GMYLMYDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNT
 130 GMYLMLDVVANHASYGGPGGSTDFSIFTPFDSASYPHSYCAINNYDNQWQVENCFLGGDDT
 251 VLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLG
 VSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGE
 Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Lipomycetaceae, Lipomyces.
 "Cloning and expression of Lipomyces starkeyi alpha-amylase in Escherichia coli and determination of some of its properties."; FEMS Microbiol. Lett. 233:53-64 (2004).
EMBL; AXISS463, AAN75021.1; -- HSSP; P26827; 1A47.
 STRAIN=KSM 22M;
PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
Moon T.-W.;
 Length 647;
 SMART; SM00642; Aamy; 1.
SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;
 Last sequence update)
Last annotation update)
 61.9%; Score 1662; DB 2; 61.4%; Pred. No. 3.8e-107;
 GO; GO:0004556; F:alpha-amylase activity; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR006047; Alpha amyl cat. InterPro; IPR006589; Alpha amyl cat. InterPro; IPR006589; Alpha amyl cat. InterPro; IPR006589; CBM 21. Pfam; PF00128; Alpha-amylase; 1. Pfam; PF00128; CBM 21; 1.
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 PRELIMINARY;
 491 GSKIC 495
 490 GSGLC 494
 Lipomyces starkeyi
 Best Local Similarity
 SEQUENCE FROM N.A.
 Alpha-amylase.
 Q6YF33;
05-JUL-2004
 05-JUL-2004
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 Query Match
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 244 KVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPRFAK 303
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 NVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFAS 323
 83
 63
 GYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVV
 204 KNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQ
 4 ASWRIQSIYFLLIDREGRIDNSTTATCNIGNEIYCGGSWQGIIDHLDYIEGMGFTAIWIS
 84 PVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHM
 SANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYTLSL
 ADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWIT
 Gaps
 Gaps
 SGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGS 478
 SGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
 Boase N.A., Murphy R.L., Kelly J.M.;
Boase N.A., Murphy R.L., Kelly J.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY Belongs to family 13 of glycosyl hydrolases.

EMBL, AF208214; APA1000.1;

R HSSP; P56211; 2AAA.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

R GO; GO:0005975; P:catbohydrate metabolism; IEA.

InterPro; IPR006047; Alpha_amyl_cat.

R InterPro; IPR006047; Alpha_amyl_cat.

R InterPro; IPR006046; Glyco_hydro_CBD.

R Pfam; PF00128; Alpha_amylase; 1.

R Pfam; PF00128; Alpha_amylase; 1.

R Pfam; PR00128; Alpha_amylase; 1.

R Pfam; PR00128; Alpha_amylase; 1.

R Pfam; PR00128; Alpha_amylase; 1.

R ProDom; P0001569; Glyco_hydro_CBD; 1.
 .
 1;
 ; Score 1725.5; DB 2; Length 623; ; Pred. No. 1.4e-111; 68; Mismatches 107; Indels 1;
 Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
 94; Indels
 68598 MW; 822F002C37F5A9A4 CRC64;
 Last sequence update)
Last annotation update)
 2.2e-115;
 623 AA
 63; Mismatches
 Pred. No.
 Created)
 PRT;
 64.3%;
66.98;
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
 Matches 318; Conservative
 Query Match
Best Local Similarity 63.73
Matches 309; Conservative
 PRELIMINARY;
 Best Local Similarity
 SEQUENCE FROM N.A.
 Alpha-amylase.
 Name=amyB;
 304
 144
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60.7%;
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292; Conservative
 377
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268
268
 JC4510; JC4510.
 587 6
304 3
344 3
624 AA;
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DOMAIN
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DISULFID
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 281
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 IQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERG 131
 MYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTV 191
 311
 402 FDGDPSYTCPYQENLDGVLAYPVYXPVVSAFESVSGSVSSLVDMIDTLKSECTDTTLLGS 461
 FVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSG:371
 YPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSN 431
 KCASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAG 491
 222 IQGMGFTAIWISPIVENIPDDTGYGYAYHGYWMKDIFALNTNFGTADDLIALATBLHNRG
 522 YSTTSTFYKYIASLNQIRNQAIYKDDTYLTYQNWVIYSDSTTIAMRKGFTGNQIITVLSN
 LGTSGSSYTLTLSNTGYTASSVVYEILTCTAVTVDSSGNLAVPMSSGLPKVFYQESQLVG
 SLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEV
 LDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGT
 Steyn A.J.C., Pretorius I.S.;
"Characterization of a novel alpha-amylase from Lipomyces kononenkoae and expression of its gene (LKA1) in Saccharomyces cerevisiae.";
Curr. Genet. 28:526-531(1995).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in Oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
 12 LQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDY
 Gaps
 MEDLINE=96105202, PubMed=8529895, DOI=10.1016/0378-1119(95)00633-0; Steyn A.J.C., Marmur J., Pretorius I.S.; "Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lipomyces kononenkoae alpha-amylase-encoding gene."; Gene 166:65-71(1995).
 Lipomyces kononenkoae.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Lipomycetaceae; Lipomyces.
2;
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan)
Name=LKA1;
110;
Mismatches
 STRAIN=IGC4052B;
MEDLINE=96132108; PubMed=8593683;
75;
Conservative
 SKICS 496
 śgics 646
 SEQUENCE OF 29-44.
 FROM N.A.
 NCBI_TaxID=34357;
 STRAIN-IGC4052B;
 432
 582
 72
 642
 132
 192
 252
 312
 372
 492
 SEQUENCE
 RESULT 15
AMY1_LIPKO
ID AMY1_LIPKO
DT 10-OCT-ID 10-OCT-ID ID 10-OCT-ID ID ID ID-OCT-ID ID ID-OCT-ID ID ID-OCT-ID ID ID-OCT-ID ID ID-OCT-ID ID ID-OCT-ID ID-O
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ö
 134
 202 MGFTAIWISPIVENIPDDTGYGYAXHGYWMKDIFALNTNFGGADDLIALATELHNRGWYL 261
 262 MVDIVVNHFAFSGNHADVDXSEYFPXSSQDYFHSFCWITDXSNQTNVEECWLGDDSVPLV 321
 254
 142 SASVPTGTAANWRGRSIYQVVTDRFARTDGSITYSCDVTDRVYCGGSYRGIINMLDYIQG 201
 135 MVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLP 194
 314
 441
 NHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPT 374
 74
 15 AAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQG
 75 MGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYL
 DLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDG
 DPAYTCPYONVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVE
 382 DPSYTCPYQENLDGVLNYPVXYPVVSAFQRVGGSISSLVDMIDTLKSECIDTTLLGSFLE
 442 NQDNPRFPSYTSDESLIKNAIAFTILSDGIPIIYYGQEQGLNGGNDPYNREALWPTGYST
 Gaps
 protein sequencing;
 similarity).

Calcium 2 (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GloNAc. ..) (Potential).
N-linked (GloNAc. ..)
 (B
 (By
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
 .
0
 similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen)
 By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
 Length 624;
 Alpha-amylase 1.
Carbohydrate binding type-21
Nucleophile (By similarity).
 Proton donor (By similarity)
 ; Score 1629; DB 1; Length 6; Pred. No. 7.1e-105; 77; Mismatches 113; Indels
 87EB16534F5A9A9F CRC64;
 metabolism; Direct
 Hydrolase; Signal
 InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR005036; CBM_21.
 Pfan; Proot290, CBM 21.
Pfan; Proot28; Alpha-amyTase; 1.
Pfan; Proot370; CBM 21; 1.
SMART; SN00642; Aamy; 1.
Calcium-binding; Carbohydrate metal Glycoprotein; Glycosidase; Hydrolas SIGNAL
 EMBL; U30376; AAC49622.1; ALT_INIT
 68876 MW;
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8 6 8 6 8 6
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<sup>495</sup> CS 496 || 622 CS 623

Search completed: February 8, 2005, 18:41:52 Job time : 300.263 secs